GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:24:53 ; Search time 7717 Seconds
                                  (without alignments)
                                  12162.347 Million cell updates/sec

Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac..........aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
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                 11: gb_htc:*
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                 16: em_estom:*
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                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1874	59.6	2172	29	AY402621	AY402621 Homo sapi
	2	1765.4	56.2	2133	29	AY402622	AY402622 Pan trogl
	3	1747.4	55.6	3206	11	AK077976	AK077976 Mus muscu
	4	1701.4	54.1	3086	11	AK035918	AK035918 Mus muscu
	5	1372.2	43.7	2172	29	AY402623	AY402623 Mus muscu
c	6	950.6	30.2	1114	13	BX367242	BX367242 BX367242
c	7	927.8	29.5	1201	13	BX363741	BX363741 BX363741
c	8	874.4	27.8	922	13	BX350606	BX350606 BX350606
	9	856.6	27.3	926	13	BX328255	BX328255 BX328255
	10	849.2	27.0	1201	13	BX384966	BX384966 BX384966
	11	827.4	26.3	974	13	BQ057192	BQ057192 AGENCOURT
	12	822.2	26.2	960	13	BX390196	BX390196 BX390196
c	13	779.8	24.8	797	14	CB243787	CB243787 UI-CF-FN0
	14	775	24.7	801	13	BX112994	BX112994 BX112994
	15	769.8	24.5	912	13	BQ883972	BQ883972 AGENCOURT
	16	768	24.4	1201	13	BX376660	BX376660 BX376660
	17	757.6	24.1	892	14	CD107028	CD107028 AGENCOURT
	18	748.6	23.8	951	13	BQ056228	BQ056228 AGENCOURT
	19	696.6	22.2	775	9	AU122156	AU122156 AU122156
	20	691.2	22.0	970	13	BQ707628	BQ707628 AGENCOURT
	21	681	21.7	1066	12	BM806752	BM806752 AGENCOURT
	22	673	21.4	1090	13	BX367243	BX367243 BX367243
	23	661.8	21.1	666	12	BG684636	BG684636 602635914
	24	650	20.7	925	13	BQ937439	BQ937439 AGENCOURT
c	25	627.4	20.0	640	14	CA311774	CA311774 UI-CF-FN0
c	26	612	19.5	624	12	BM666780	BM666780 UI-E-CL1-
	27	609.8	19.4	1119	12	BI550650	BI550650 603195823
	28	598.6	19.0	621	10	AW965845	AW965845 EST377918
c	29	598.4	19.0	634	13	BU632880	BU632880 UI-H-FE1-
c	30	594	18.9	618	13	BU686374	BU686374 UI-CF-DU1
	31	585.2	18.6	881	13	BQ960065	BQ960065 AGENCOURT
	32	579.2	18.4	720	14	CA315771	CA315771 UI-M-FW0-
	33	557.8	17.7	796	13	BU052878	BU052878 UI-M-FC0-
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	35	552.4	17.6	779	12	BI683727	BI683727 603306287
	36	551.4	17.5	695	12	BG685741	BG685741 602637838
	37	547	17.4	547	12	BM128651	BM128651 if14b09.y
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	42	528	16.8	528	14	CA393520	CA393520 cs39b03.y
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RESULT 1
AY402621

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DEFINITION  Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY402621
VERSION     AY402621.1  GI:39758607
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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                     /mol_type="genomic DNA"
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  Best Local Similarity  86.3%;  Pred. No. 0;
  Matches 1874;  Conservative   0;  Mismatches  298;  Indels   0;  Gaps    0;
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Qy     105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
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Qy     165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 224
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Db      61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 120
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Qy     225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Qy     285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Qy     345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
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Qy     405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Qy     465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Qy     645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
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Qy     705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
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Db     601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 660

Qy     765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
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Db     661 GACAACTTCCTCCGCTGGCTGCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy     825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884
Db     721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy     885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944
Db     781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

Qy     945 AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC 1004
Db     841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900

Qy    1005 TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC 1064
Db     901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960

Qy    1065 TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1124
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Qy   1125  TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1184
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Db   1021  TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1080

Qy   1185  ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 1244
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Qy   1485  CAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA 1544
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Qy   1545  GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT 1604
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Qy   1605  GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC 1664
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Qy      2145 TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2204
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Qy      2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAG 2264
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Db      2101 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAG 2160

Qy      2265 ACCCTGCGCCCT 2276
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DEFINITION  Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY402622
VERSION     AY402622.1  GI:39758608
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 2133)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2133)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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ORIGIN

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Qy        225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Db        121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy        285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Qy        405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Db        301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy        465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Qy        525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
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Qy        585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
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Qy        645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
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Db        541 GCTCACAAGCATACGGCTGTCTTGGTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600

Qy        705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
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Qy     765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC  824
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Qy    1305 CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG 1364
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Db    1261 GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 1320

Qy    1425 GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 1484
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Db    1321 GGGTCGNTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGANNNNNTT 1380

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Qy   1605  GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC  1664
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Db   2101  ATCCTCNTGGCCTCCCCANNGAGAGCACTCCGG  2133


RESULT 3
AK077976
LOCUS       AK077976                3206 bp    mRNA    linear    HTC 18-SEP-2003
DEFINITION  Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
            enriched library, clone:6030492A12 product:sema domain,
            immunoglobulin domain (Ig), transmembrane domain (TM) and short
            cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION   AK077976
VERSION     AK077976.1  GI:26097602
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
    TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
    TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
    TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
    TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
    TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6   (bases 1 to 3206)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
    TITLE   Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

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                RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                Fax:81-45-503-9216)
COMMENT         cDNA library was prepared and sequenced in Mouse Genome
                Encyclopedia Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                Division of Experimental Animal Research in Riken contributed to
                prepare mouse tissues.
                Please visit our web site for further details.
                URL:http://genome.gsc.riken.go.jp/
                URL:http://fantom.gsc.riken.go.jp/.
FEATURES                 Location/Qualifiers
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                         domain (TM) and short cytoplasmic domain, (semaphorin) 4A
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                         /note="putative"
     polyA_site          3206
                         /note="putative"
ORIGIN

  Query Match              55.6%;  Score 1747.4;  DB 11;  Length 3206;
  Best Local Similarity    76.7%;  Pred. No. 0;
  Matches 2355;  Conservative   0;  Mismatches  621;  Indels  95;  Gaps   14;


Qy         75 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCC 134
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Db        194 GAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCA 253

Qy        135 TGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACC 194
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Db        254 TGGAGTCTCCTGCGTGTTTTTTTCTTCCAACTCTTCCTGCTGCCATCACTGCCACCTGCT 313

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Qy    315 GGTGATGGAAATACTCTCTACGTGGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAG 374
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Qy    495 CTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCT 554
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Qy    555 TGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATG 614
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Db   2171 CCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGG 2230

Qy   2114 TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT 2173
          || || || |||||||||||| |||||||||||||| ||| ||| || || |||||
Db   2231 CGGAGCTTCCATGGCTGCCCAGCGGTCCTACTGGCCCCATTTTCTCATCGTTACCGTCCT 2290

Qy   2174 CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
          | | ||| | |||||    |||| |||| |||||| | || |||||| || | || ||
Db   2291 CCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCT 2350

Qy   2234 CCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTT 2293
          |||||||||||| |||||||||||||||||| || |||| ||| |||| ||||| || |
Db   2351 GCGGGCTCGGGGTAAGGTTCAGGGCTGTGGGATGCTGCCCCCCAGGGAAAAGGCTCCACT 2410

Qy   2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2353
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Db   2411 GAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGA 2470

Qy   2354 CGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCT- 2412
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Qy   2413 -GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATG 2471
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Db   2531 AGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC-------------------------- 2563

Qy   2472 ACAGCAGCACAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACT 2531
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Qy   2532 GATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACC 2591
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Db   2620 TACAGCACCCAGTAGG------------------TCCTCCCCTGTGGGACTCTCTTCTGCA 2662

Qy   2592 AAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATAT 2651
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Qy   2652 TGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAG 2711
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Db   2704 AGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTCCTGTAACAAAC 2763

Qy   2712 TGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAA 2771
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Qy   2772 CATCTAAACAATCATATGCTA-------ACATGCCACTCCTGGAAACTCCACTCT----G 2820
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Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCC 2879
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Qy    2880 CTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTG 2939
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Db    2943 CTTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTA 2999

Qy    2940 ACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGC-AG 2995
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Db    3000 ACCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAG 3059

Qy    2996 AATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCT 3055
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Qy    3056 CCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTT 3115
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RESULT 4
AK035918

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LOCUS       AK035918                3086 bp    mRNA    linear   HTC 19-SEP-2003
DEFINITION  Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:9630018D15 product:sema domain,
            immunoglobulin domain (Ig), transmembrane domain (TM) and short
            cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION   AK035918
VERSION     AK035918.1  GI:26084904
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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                Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
                sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
    PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
                FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
                Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
                of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3086)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
                Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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                Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
                Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
                Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
                Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
                Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
                Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
                Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
                Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                Physical and Chemical Research (RIKEN), Laboratory for Genome
                Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                Fax:81-45-503-9216)
  COMMENT   cDNA library was prepared and sequenced in Mouse Genome
                Encyclopedia Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                Division of Experimental Animal Research in Riken contributed to
                prepare mouse tissues.
                Please visit our web site for further details.
                URL:http://genome.gsc.riken.go.jp/
                URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
     source   1. .3086
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                     /strain="C57BL/6J"
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       misc_feature     59. .2388
                        /note="putative
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                        domain (TM) and short cytoplasmic domain, (semaphorin) 4A
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                        match=2517)"
       polyA_signal     3062. .3067
                        /note="putative"
       polyA_site       3086
                        /note="putative"
ORIGIN

     Query Match              54.1%;   Score 1701.4;   DB 11;   Length 3086;
     Best Local Similarity    75.2%;   Pred. No. 0;
     Matches 2364;  Conservative     0;  Mismatches   637;  Indels  141;  Gaps    14;

Qy         50 AACGCAGCGGCATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGC 109
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Db          4 AACCCAGAAAGTGCCTGTTTCCTCAGAACCATCTGGTGACCATCTCAGGCTGACCATGGC 63

Qy        110 CCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCT 169
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Qy        170 TCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGT 229
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Qy        230 CAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCA 289
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Db        184 CAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAAGGCCTCCG 243

Qy        290 GGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGA 349
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Qy        350 AGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACC 409
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Qy        470 ACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTG 529
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Qy        530 CGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATT--------------------- 566
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Db        484 TGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTACGTGCGACCCTGGCATTCTGGG 543

Qy        567 ----------------------GAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAG 602
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Db        544 CTCCCAGCCTCTTCCCCCCTCTAGGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATA 603
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Qy    603  GACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCT  662
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Qy    663  GTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCC  722
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Db    664  GTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGCGAGCCC  723

Qy    723  ATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGG  782
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Qy    783  CTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTC  842
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Qy    843  TTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCT  902
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Db    844  TTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCT  903

Qy    903  AGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC  962
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Db    904  CAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC  963

Qy    963  CTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCAC  1022
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Qy    1023 GCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCC  1082
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Qy    1083 CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATT  1142
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Qy    1143 GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACT  1202
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Qy    1203 TATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGAT  1262
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Qy    1323 CTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTT  1382
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Qy    1443 GTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCT  1502
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Qy    2283 AAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCC 2342
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                         |||    |  | |   ||  |     |   ||||  || ||||||
Db   2445 ---------------CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAA 2489

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
          || |||| |   ||| ||| |||                    |||||||| ||||||
Db   2490 CGTGTGTCACCTACAGCACCCAGTAGGT----------------CCTCCCCTGTGGGAC 2532

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          || ||||| | |       || ||| |||                 ||| ||||| |
Db   2533 TCTCTTCTGCAAGCACATTGGGCTGTCT-------------------CCATACCTGTACT 2573

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
          |   ||| |  |  | | | || ||| | ||  ||  || ||       ||| |  |||||
Db   2574 TGTGCTGTGACAGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTC 2633

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
          | | ||||| |    || ||    ||  ||   |||           |  ||| || ||||| |
Db   2634 CTGTAACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGA 2693

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTA-------ACATGCCACTCCTGGAAACTC 2813
          ||| | || |||| | ||| |  |||        ||||        | |  ||| |
Db   2694 CAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCCTGCAAACTCCATCCTGAACGCTGT 2752

Qy   2814 CACTCT----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAG 2868
          ||||||      |  ||||||| |||||| ||||||| | | |||| | ||||| |    | |
Db   2753 CACTCTAGAAGCAGCTGCTGCTTTGAACACCAGCCCACCCTCCTTCCCAAGAGTCTCTAT 2812

Qy   2869 GGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTT 2928
          |||  || |||| || ||||  |||||||||||| |||   ||| |   |||||||| |
Db   2813 GGAGTTGGCCCCTTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATC 2869

Qy   2929 CCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCT 2985
          |||||||| |||||||| |||||||||||||||||||| || |||| | | ||  |   |||
Db   2870 TCTGAAGTCTAACCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCT 2929

Qy   2986 GCCCTGGC-AGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACC 3044
          ||||||||| |||||||  ||  ||||||||||||||||| ||| ||  |  | | |||||||
Db   2930 GCCCTGGCTAGAATGGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCCAGTGTGGCTGACC 2989

Qy   3045 CCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAG 3104
          | |  |  | | || ||| | |||||||||| ||||||||||||||||||||||||||| ||
Db   2990 CTTGACCTCTT--CCTTCCTCCTCCCTTTGTTTGGGGATTCAGAAAACTGCTTGTCACAG 3047

Qy   3105 ACTGTTTATTTTTTATTAAAAA 3126
          || |||||||||||||||||||
Db   3048 ACAATTTATTTTTTATTAAAAA 3069
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RESULT 5
AY402623

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LOCUS           AY402623                2172 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY402623
VERSION     AY402623.1  GI:39758609
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2172
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>2172
                     /locus_tag="HCM1285"
ORIGIN
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Query Match              43.7%;  Score 1372.2;  DB 29;  Length 2172;
Best Local Similarity    71.9%;  Pred. No. 0;
Matches 1560;  Conservative    0;  Mismatches  611;  Indels    0;  Gaps    0;


Qy     105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
               ||||||||| ||| |||||||||| |||| | ||||| |||||| |  |||| |||||||||
Db       1 ATGGCCCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTTCTTCCAA 60

Qy     165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCC 224
               ||  | | |||||     | | |  |  | | |||   || || |||||||||||||||||
Db      61 CTCTTCCTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCC 120

Qy     225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
               || |||| |||| |||| || || |  |  |||||| || |||||||||||||| || ||| |||
Db     121 AGAGTCAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGC 180
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Qy     285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
           ||||   || ||||||||| |||||||||||||  ||||| || ||||||||| |||||||||||
Db     181 CTCCGAGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCT 240

Qy     345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
           ||||| ||| | |||||||||| |||||||| | ||||| |||| |||||||||||||||||||||
Db     241 CGAGAGGCCGTCCTGGCCTTGAATATCCAGAACCCAGGAATCCCAAGGCTAAAGAACATG 300

Qy     405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
           |||||  |||||||||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     301 ATACCCTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy     465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
           |||||||||||||||||||||||| || ||||||||| |||||||||| || || ||||||
Db     361 GAGACACAGTGTTTCAACTTCATTCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTAT 420

Qy     525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
           |||| || ||||| ||||||||||||||||||| |||||||||||||||||||||||||| |
Db     421 GCCTGTGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTGAACTCCAAGATTCCCTC 480

Qy     585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
           |||||||||||||| |    |||||||||||||| || || ||||||||||||||||||||||
Db     481 CTGTTGCCCATCTTGATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCCCTTTGACCCT 540

Qy     645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
           | |||||||||| || ||||||||||| |||||||||||| ||||| || || ||||||||
Db     541 GTTCACAAGCACACAGCTGTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC 600

Qy     705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGATCCCAGCCTGTCCTCAAGACC 764
           |||||||||||| ||||||||||||||||| |||||||||||||||||||| |||||||
Db     601 TTCCTGGGCAGCGAGCCCATCCTGATGCGGACACTGGATCCCAGCCTGTTCTCAAGACT 660

Qy     765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
           |||| |||| | |||||||||||||
Db     661 GACATCTTCTTACGCTGGCTGCACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy     825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884

Db     721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy     885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944

Db     781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

Qy     945 AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC 1004

Db     841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900

Qy    1005 TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC 1064

Db     901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960

Qy    1065 TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1124
                                              |||||||||||||||||||||||| || || ||||||
Db     961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNGCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCC 1020
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Qy   1125 TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1184
           ||||||||| |||||||||| || |||||||| ||||| ||||| ||| ||||||| ||
Db   1021 TTCTCTCTCACGGACATTGAGCGAGTCTTTAAAGGGAAGTACAAGGAGCTGAACAAGGAG 1080

Qy   1185 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 1244
           || || ||||||||| ||||| ||||| | ||| || ||| ||||||||||||||||||
Db   1081 ACCTCCCGCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCGAGGCCAGGCAGTTGCTCC 1140

Qy   1245 GTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG 1304
           |||||||||||||| || ||| |||||||||||||||||||||||| |||||||||||||
Db   1141 ATGGGCCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTTCTGATGGATGAG 1200

Qy   1305 CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG 1364
           || ||||| || || |||||||||||||||| ||| ||||||||| ||||||||| |||
Db   1201 CACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTG 1260

Qy   1365 GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 1424
           ||| ||||| | ||||||||||||| |||||||| | ||||||| ||||| ||| ||||
Db   1261 GAGTCAGCTCGGGGCCTTGATGGGAGCAGCCATGTGGTCATGTATCTGGGTACCTCCACG 1320

Qy   1425 GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 1484
           ||||| || |||||||||||||| |  | ||||||||||||| |||| ||||| ||||||
Db   1321 GGGTCCCTGCACAAGGCTGTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATT 1380

Qy   1485 CAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA 1544
           ||||||  ||||||| ||||| |||||||| ||||||||||||||||||| |||||||||
Db   1381 CAGCTGAGCCCTGACTCTGAGCCTGTTCGAAACCTGCAGCTGGCCCCCGCCCAGGGTGCA 1440

Qy   1545 GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT 1604
           ||||||| ||||||||| |||||| |||  ||||| || ||| |||||| || ||||||
Db   1441 GTGTTTGCAGGCTTCTCTGGAGGCATCTGGAGAGTTCCCAGGGCCAATTGCAGTGTCTAC 1500

Qy   1605 GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC 1664
           |||||||||||||||||||||| |||| ||||||| ||||||||||||||||||||| ||
Db   1501 GAGAGCTGTGTGGACTGTGTGCTTGCCAGGGACCCTCACTGTGCCTGGGACCCTGAATCA 1560

Qy   1665 CGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG 1724
           ||  |||  |||| ||||||| | | |  |  |   | |||||||||||||||||| ||
Db   1561 AGACTCTGCAGCCTTCTGTCTGGCTCTACCAACAGGCCTTGGAAGCAGGACATGGAACGC 1620

Qy   1725 GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC 1784
           || ||||| ||||||| ||||| ||  || |||||||||||| ||||||| |||||||||
Db   1621 GGCAACCCGGAGTGGGTATGCACCCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGC 1680

Qy   1785 CGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC 1844
           | ||| ||| | ||||||||||||||| | ||||||||||||||||||||||| ||||||
Db   1681 CCCCCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGC 1740

Qy   1845 CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA 1904
           |||||||||||||| ||||||||||| ||||||||||||||||| || | || |||||
Db   1741 CCCCACCTGTCAGCACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAA 1800

Qy   1905 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT 1964
           ||||| | || ||||||||||||||||||||||||||| |  |||||||| || |||||
Db   1801 GCCTCTGCTACCGTCTACAATGGCTCCCTCTTGCTGCTGCCGCAGGATGGTGTCGGGGGC 1860

Qy   1965 CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG 2024
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              ||||||||||    ||| |||||||||| ||||  |||||||||||||| ||||||| |||||
Db      1861  CTCTACCAGTGTGTGGCGACTGAGAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTA 1920

Qy      2025  GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT 2084
              |||||||||||||||| |||||||| ||||| ||||| ||||| ||| | ||||| |||| |
Db      1921  GACAGCCAGGACCAGCCCCTGGCGCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGT 1980

Qy      2085  GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC 2144
              ||| ||||||||| |||||||||||| | || || || || |||||||||||| |||||||
Db      1981  GTGCAGGTCCCGCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCCAGCGGTCCTAC 2040

Qy      2145  TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2204
              ||||||||| ||| ||| || || |||||| | ||| | |||||     |||| ||||
Db      2041  TGGCCCCATTTTCTCATCGTTACCGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACT 2100

Qy      2205  ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAG 2264
              ||||| | || |||||| || | || || |||||||||||| ||||||||||||||| |
Db      2101  CTCCTCCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGGTTCAGGGCTGTGGG 2160

Qy      2265  ACCCTGCGCCC 2275
              |  |||| |||
Db      2161  ATGCTGCCCCC 2171


RESULT 6
BX367242/c
LOCUS       BX367242               1114 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX367242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL002YO04 3-PRIME, mRNA sequence.
ACCESSION   BX367242
VERSION     BX367242.1  GI:30455608
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AL002BH02NP1&cluster=907.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AL002BH02NP1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                   /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                   25-NORMALIZED"
                   /note="1st strand cDNA was primed with a NotI-oligo(dT)
                   primer. Five prime end enriched, double-strand cDNA was
                   digested with Not I and cloned into the Not I and EcoR V
                   sites of the pCMVSPORT 6 vector. Library was normalized."
          ORIGIN

            Query Match            30.2%;  Score 950.6;  DB 13;  Length 1114;
            Best Local Similarity  94.8%;  Pred. No. 1.7e-220;
            Matches  996;  Conservative  24;  Mismatches  27;  Indels  4;  Gaps  4;
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Qy        2073 CCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCC 2132
               |||| ||||||||||| |||||||||||||||||:|||||||||| :||||:|||||||||||
Db        1055 CCCCCGGAGCATGT-AAGGTCCCGTTGACMAGGGTCAGTGG-KGGGCSGCCCTGGCTGCC 998


Qy        2133 CAGCAGTCCTACTGGCCCC-ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTC 2191
               |||:||||::|||| ||||| ||||||| ||||| |||||||||||||||| |||||||||
Db         997 CAGMAGTCMYACTTGCCCCAACTTTGTAACTGTAACTGTCCTCTTTGCCTAAGTGCTTTC 938


Qy        2192 AGGAGCCCTCATCATCCTCGTGGCCTCCCC-ATTGAGAGCACTCCGGGCTCGGGGCAAGG 2250
               |||||||||||||||||||||||||||||| ||||||||:||||||||||||| ||||||
Db         937 AGGAGCCCTCATCATCCTCGTGGCCTCCCCAATTGAGAGMACTCCGGGCTCGGCGCAAGG 878


Qy        2251 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACC 2310
               ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         877 TTMAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACC 818


Qy        2311 TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCC 2370
               |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db         817 TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTAACAACAACTGCC 758


Qy        2371 TAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGC 2430
               ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db         757 TAGGCACTGAGGTMGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGC 698


Qy        2431 CATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCA 2490
               ||||||||||||||||||||||:|||||||||||||||||:|||||||||||||||||||||
Db         697 CATGCTGGCTGGGCGGCCCAAGMACAGCCCTGACTAGGATSACAGCAGCACAAAAGACCA 638


Qy        2491 CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG 2550
               |||||||||||||||||||||||||||||||||||||||:||||||:||||||||||||||
Db         637 CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATMACTGATVACACTCAGCAGGGTG 578


Qy        2551 ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAA 2610
               ||| |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         577 ATGAACAGCAGTCTGCCTCCCCTATGGAACTCCCTTCTACCAAGCACATGAGCTCTCTAA 518


Qy        2611 CAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGAT 2670
               ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         517 CAGGGTGGGGGCTACCCCCAGACCTGCTCCTAAACTGATATTGAAGAACCTGGAGAGGAT 458


Qy        2671 CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA 2730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       457  CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA  398

Qy      2731  AAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGC  2790
              ||||||||:|||||||||||||||||||||||||||||||||||||||||| ||| ||||||
Db       397  AAACCTGCMTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAAAAATAATATGC  338

Qy      2791  TAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT  2850
              |||:|||| ||||||||||||||:|:||||||||||||||||||| |:||||| |||||||
Db       337  TAAMATGCAACTCCTGGAAACTCMAMTCTGAAGCTGCCGCTTTGAAMACCAAAACTCCCT  278

Qy      2851  TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCT  2910
              ||||||||||||||:|||||||||||||||||||||||||||||||:|||||||:|| |||
Db       277  TCTCCCAGGGTCATGMAGGGATCTGCTCCCTCCTGCTTCCCTTACMAGTCGTGMACAGCT  218

Qy      2911  GACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAG  2970
              ||||||||||||||| ||||||||||||||||||||||| ||| |||| |||||||:| |
Db       217  AACTCCCAGGAAGTCTTCCCTGAAGTCTGACCACCTTTCNTCTAGCTTAAGTTGGRGAAA  158

Qy      2971  ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTT  3030
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||
Db       157  ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATNGAGCCTTCTTAACTCCTT  98

Qy      3031  TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAA  3090
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        97  TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAA  38

Qy      3091  ACTGCTTGTCAGAGACTGTTTATTTTTTATT  3121
              ||||||||||||||||||||||| ::|||| ||
Db        37  ACTGCTTGTCAGAGACTGTTTCBYTTTTCTT  7
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RESULT 7
BX363741/c

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LOCUS       BX363741                1201 bp    mRNA    linear    EST 05-MAY-2003
DEFINITION  BX363741 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.
ACCESSION   BX363741
VERSION     BX363741.1  GI:30384744
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DL005AB09NP1&cluster=907.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
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FEATURES   Location/Qualifiers
    source   1. .1201
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="CS0DL005YC17"
                  /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                  /cell_line="RAMOS CELL LINE"
                  /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                  25-NORMALIZED"
                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
                  primer. Five prime end enriched, double-strand cDNA was
                  digested with Not I and cloned into the Not I and EcoR V
                  sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match   29.5%; Score 927.8; DB 13; Length 1201;
  Best Local Similarity   95.4%; Pred. No. 6.6e-215;
  Matches 1001; Conservative   16; Mismatches   24; Indels   8; Gaps   6;

Qy   2058 GAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGG 2117
            || ||| |||| | || | | : |:|||||||||||| :|||||||||||||
Db   1042 GATCTGAATGGCAGCATCCCCGGGAGMWGKGARGTCCCGTTGACC-RGGTCAGTGGTGGG 984

Qy   2118 GCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTT 2177
            | || | | :|||||||||||||:|:|| ||| |||||||||||||||||||||||||
Db   983 --CCGCCCTGGYGCCCAGCAGTCCWAYTG--CCCCATTTGTCACTGTCACTGTCCTCTTT 928

Qy   2178 GCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237
            ||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||
Db   927 GCCTTAGTGCTTTCA-GAGCCCTCATCATCCTCGT-GCCTCCCCATTGAGAGCACTCCGG 870

Qy   2238 GCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 2297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869 GCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 810

Qy   2298 AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 2357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809 AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 750

Qy   2358 GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   749 GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 690

Qy   2418 GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA 2477
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   689 GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA 630

Qy   2478 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 2537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   629 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 570

Qy   2538 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 2597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   569 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 510

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Qy    2598 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 2657
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 450

Qy    2658 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 2717
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 390

Qy    2718 AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA 2777
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA 330

Qy    2778 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 2837
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 270

Qy    2838 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 2897
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 210

Qy    2898 GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT 2957
           |||||||||||||||||||:|||||||||||| ||||||:|||||||||||||||||||
Db     209 GTCGTGCACCGCTGACTYCCAGGAAGTCTTCCCTGAAKTCTGACCACCTTTCTTCTTGCT 150

Qy    2958 TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG-CAGGGGTAATCTGAGC 3016
           |||||||||||||:|:||||||||||||||||||||:|||||||| |||||||||||||||
Db     149 TCAGTTGGGGCAGAYTYTGATCCCTTCTGCCCTGGYAGAATGGTCAGGGGTAATCTGAGC 90

Qy    3017 CTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTT 3076
           |||||||||||||||||||||||||||||||||||||:|||||||||:|::||||||||||
Db      89 CTTCTTCACTCCTTTACCCTAGCTGACCCCTTCMCCTCTCCCCBTSSCTTTTCCTTTGTT 30

Qy    3077 TTGGGATTCAGAAAACTGCTTGTCAGAGA 3105
           |||||||||||||||||||||||||||:|
Db      29 TTGGGATTCAGAAAACTGCTTGTCAGAKA 1
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RESULT 8
BX350606/c
LOCUS   BX350606   922 bp   mRNA   linear   EST 05-MAY-2003
DEFINITION   BX350606 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
             Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.
ACCESSION   BX350606
VERSION   BX350606.1 GI:30373499
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 922)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France

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FEATURES                Location/Qualifiers
     source             1. .922
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0DL005YC17"
                        /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                        /cell_line="RAMOS CELL LINE"
                        /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                        25-NORMALIZED"
                        /note="1st strand cDNA was primed with a NotI-oligo(dT)
                        primer. Five prime end enriched, double-strand cDNA was
                        digested with Not I and cloned into the Not I and EcoR V
                        sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

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   Query Match            27.8%;   Score 874.4;   DB 13;   Length 922;
   Best Local Similarity  98.7%;   Pred. No. 6.3e-202;
   Matches  878;  Conservative   0;  Mismatches  12;  Indels   0;  Gaps    0;


Qy     1372 CCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGC 1431
            |||||| |||||||||||||||||||||||||||||||||| ||||||||| |||||||||
Db      919 CCCAGGNCCTTGATGGGCACAGCCATCTTGTCATGTACTTGGGAACCACAACAGGGTCGC 860


Qy     1432 TCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGT 1491
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      859 TCCACAAGACTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGT 800


Qy     1492 TCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTG 1551
            ||||||||||||| |||||||||||||||||||||||||| ||||| ||||||||||||||
Db      799 TCCCTGACCCTGANCCTGTTCGCAACCTGCAGCTGGCCNCCACCAAGGGTGCAGTGTTGN 740


Qy     1552 TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCT 1611
            |||||||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Db      739 TAGGCTTCTCAGNAGGTGTCTGGAGGGTGCNCCGAGCCAACTGTAGTGTCTATGAGAGCT 680


Qy     1612 GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT 1671
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      679 GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT 620


Qy     1672 GTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC 1731
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      619 GTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC 560


Qy     1732 CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC 1791
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      559 CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC 500
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Qy     1792 AAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACC 1851
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      499 AAATCATTAAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCCACC 440

Qy     1852 TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT 1911
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      439 TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT 380

Qy     1912 CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC 1971
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      379 CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC 320

Qy     1972 AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC 2031
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      319 AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC 260

Qy     2032 AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGG 2091
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      259 AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGG 200

Qy     2092 TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC 2151
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      199 TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC 140

Qy     2152 ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG 2211
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      139 ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG 80

Qy     2212 TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGT 2261
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       79 TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGT 30
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RESULT 9
BX328255

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LOCUS       BX328255                 926 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.
ACCESSION   BX328255
VERSION     BX328255.1  GI:30307730
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG053ZH06_C
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FEATURES                Location/Qualifiers
     source             1. .926
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0DL005YC17"
                        /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                        /cell_line="RAMOS CELL LINE"
                        /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                        25-NORMALIZED"
                        /note="1st strand cDNA was primed with a NotI-oligo(dT)
                        primer. Five prime end enriched, double-strand cDNA was
                        digested with Not I and cloned into the Not I and EcoR V
                        sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

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  Query Match                27.3%;   Score 856.6;  DB 13;  Length 926;
  Best Local Similarity   98.1%;   Pred. No. 1.4e-197;
  Matches  909;  Conservative    0;  Mismatches   14;  Indels   4;  Gaps     4;


Qy       805 TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGG-AGACAGCCAGCGAG 863
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db         1 TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAAGACAGCCAGCGAG 60

Qy       864 TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG 923
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG 120

Qy       924 GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGC 983
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGC 180

Qy       984 ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT 1043
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT 240

Qy      1044 TCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACC 1103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACC 300

Qy      1104 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 1163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 360

Qy      1164 TACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC 1223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC 420

Qy      1224 CCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 1283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 480

Qy      1284 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTG 1343
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Db      481 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTG 540

Qy     1344 GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC 1403
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC 600

Qy     1404 ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT 1463
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Db      601 ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT 660

Qy     1464 GCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAG 1523
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAG 720

Qy     1524 CTGGCCCCCACCCAGGGTGCA-GTGTTTGTAGGCTTCTCAGGAGGTGTCTGG-AGGGTGC 1581
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Db      721 CTGGCCCCCACCCCAGGTGCANGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGNAGGGTGC 780

Qy     1582 CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCC 1641
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db      781 CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGACCCCC 840

Qy     1642 ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACT 1701
                  ||||||||||||||||||||||||||||  |||||||||||  ||||||||||||||||||   |||
Db      841 -CTGTGCCTGGGACCCTGAGTCCCGACCCTGTTGCCTTCTGTCTGCCCCCAACCTTGACT 899

Qy     1702 CCTGGAAGCAGGACATGGAGCGGGGGA 1728
                  |||  |  |     |||||||||||||  |
Db      900 CCTTGGAAGCAGACATGGAGCGGGGAA 926


RESULT 10
BX384966
LOCUS        BX384966              1201 bp    mRNA    linear    EST 08-MAY-2003
DEFINITION   BX384966 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
             Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.
ACCESSION    BX384966
VERSION      BX384966.1  GI:30436505
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 1201)
  AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE      Full-length cDNA libraries and normalization
  JOURNAL    Unpublished (2001)
COMMENT      Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 907.f For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CS0DL005AB09QP1&cluster=907.f. Contact :
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FEATURES   Location/Qualifiers
    source   1. .1201
                       /organism="Homo sapiens"
                       /mol_type="mRNA"
                       /db_xref="taxon:9606"
                       /clone="CS0DL005YC17"
                       /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                       /cell_line="RAMOS CELL LINE"
                       /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                       25-NORMALIZED"
                       /note="1st strand cDNA was primed with a NotI-oligo(dT)
                       primer. Five prime end enriched, double-strand cDNA was
                       digested with Not I and cloned into the Not I and EcoR V
                       sites of the pCMVSPORT 6 vector. Library was normalized."
    ORIGIN

  Query Match   27.0%;   Score 849.2; DB 13;   Length 1201;
  Best Local Similarity   97.0%;   Pred. No. 1e-195;
  Matches 871; Conservative   4; Mismatches   22; Indels   1; Gaps   1;

Qy   99 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 158
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 127

Qy   159 TTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCC 218
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 TTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCC 187

Qy   219 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 278
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 247

Qy   279 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 338
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   248 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGCTGATGGAAATACTCTCTACGTG 307

Qy   339 GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG 398
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   308 GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG 367

Qy   399 AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG 458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG 427

Qy   459 AGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT 518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428 AGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT 487

Qy   519 CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT 578
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488 CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT 547

Qy   579 TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT 638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db        548  TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT  607

Qy        639  GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG  698
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608  GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG  667

Qy        699  AACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC  758
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668  AACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC  727

Qy        759  AAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT  818
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728  AAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT  787

Qy        819  TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG  878
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788  TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG  847

Qy        879  AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG  938
               |||||||||||||||||||||||||||||||||||||||||||||||||||| |||:|||
Db        848  AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCG-AAARCTG  906

Qy        939  CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGC  996
               |||||||||||||||||||:|||  |    |   | | ||:   :     ||| | |   ||
Db        907  CTGCAGAAGAAGTGGACCMCCTCCTGAAGCCCACYGCYCTCMCCAGCCCGGGCACTGC  964


RESULT 11
BQ057192
LOCUS       BQ057192                 974 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6769628 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812383
            5', mRNA sequence.
ACCESSION   BQ057192
VERSION     BQ057192.1  GI:19816532
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2062  row: 1  column: 16
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
     source          1. .974
                     /organism="Homo sapiens"
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                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="IMAGE:5812383"
                         /tissue_type="lymphoma, cell line"
                         /lab_host="DH10B (phage-resistant)"
                         /clone_lib="NIH_MGC_99"
                         /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                         EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                         into EcoRI/XhoI sites using the following 5' adaptor:
                         GGCACGAG(G). Size-selected >500bp for average insert size
                         1.8kb. Library constructed by Ling Hong in the laboratory
                         of Gerald M. Rubin (University of California, Berkeley)
                         using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                         II RT (Life Technologies). Note: this is a NIH_MGC
                         Library."
ORIGIN

     Query Match                26.3%;   Score 827.4;   DB 13;   Length 974;
     Best Local Similarity   92.6%;   Pred. No. 1.9e-190;
     Matches  902;  Conservative    0;  Mismatches   67;  Indels    5;  Gaps     3;


Qy        92 TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT 151
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT 60


Qy       152 TTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA 211
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA 120


Qy       212 GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT 271
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT 180


Qy       272 CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT 331
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT 240


Qy       332 CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG 391
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG 300


Qy       392 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA 451
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA 360


Qy       452 GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT 511
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT 420


Qy       512 CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT 571
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT 480


Qy       572 TCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 631
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 540
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Qy     632 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 691
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 600

Qy     692 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC 751
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC 660

Qy     752 TGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 720

Qy     812 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT 871
           ||||||||||||||||||||||||||||||||||||||    |||||||||||||||||||
Db     721 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGGAGAGACAGCCAGCGAGTTTGACTT 780

Qy     872 CTTTGAGAGGCTCCACACATCGCGGGTGG-CTAGAGTCTGCAAGAATGACGTGGGC-GGC 929
           |||||||||||| ||   |  || |||| || ||| |||||||| | ||||||||||| |||
Db     781 CTTTGAGAGGCCCCCACCCTCCCGGGGGGCCTANAGTCTGCCAAAATGACGTGGGCGGGC 840

Qy     930 GAAAAGCTGCTGCAGAAGAA---GTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACC 986
           ||||||||||||||| || ||    | ||  || | | | ||||||||||||||||||| ||
Db     841 GAAAAGCTGCTGCAAAAAAAAGTGGACCCCCCTTCCTTGAAGGCCCAGCTGCTCTGGCCC 900

Qy     987 CAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCT 1046
           |   | ||| |          |      | || | ||| | | ||| ||      |
Db     901 CCAGCCGGGGGGAGCTTGCCCTTTCACGTCATTCCCGCCCCCGGGGTCCTGGCTCCCCCC 960

Qy    1047 CCCACAGCTCCCCA 1060
           || |    ||||||
Db     961 CCGAATTTTCCCCA 974
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RESULT 12
BX390196

LOCUS   BX390196   960 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD003YE08 5-PRIME, mRNA sequence.
ACCESSION   BX390196
VERSION   BX390196.1 GI:30463276
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 960)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/

FEATURES   Location/Qualifiers
    source   1. .960
                         /organism="Homo sapiens"
                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="CS0DD003YE08"
                         /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                         /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                         /note="1st strand cDNA was primed with a NotI-oligo(dT)
                         primer. Five prime end enriched, double-strand cDNA was
                         digested with Not I and cloned into the Not I and EcoR V
                         sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

    Query Match   26.2%;   Score 822.2;   DB 13;   Length 960;
    Best Local Similarity   97.2%;   Pred. No. 3.6e-189;
    Matches 900; Conservative   0; Mismatches   19; Indels   7; Gaps   6;

Qy   1530 CCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCC 1589
             ||| ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   10 CCCCACCAGGGTGCAGTGTTTGTAGGCTTCT-AGGAGGTGTCTGGAGGGTGCCCCGAGCC 68

Qy   1590 AACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCC 1649
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 AACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCC 128

Qy   1650 TGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAG 1709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   129 TGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAG 188

Qy   1710 CAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGC 1769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   189 CAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGC 248

Qy   1770 CTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATC 1829
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   249 CTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCTAACTCCATC 308

Qy   1830 CTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCA 1889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   309 CTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCA 368

Qy   1890 GCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAG 1949
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   369 GCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAG 428

Qy   1950 GATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTG 2009
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 GATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTG 488

Qy   2010 ATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGC 2069
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 ATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGC 548

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Qy    2070 ATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCT 2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     549 ATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCT 608

Qy    2130 GCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTT 2189
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db     609 GCCCAGCAGTCCTACTGGCCCCACTNTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTT 668

Qy    2190 TCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAG 2249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     669 TCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTTCGGGCAAG 728

Qy    2250 GTTC-AGGGCTGTGAGACCCTGCGCCCTGGGG--AGAAGGCCCCGTTAAGCAGAGAGCAA 2306
           |||| ||||||||||||||||||||||||||||    | ||||||||||||||||||||||
Db     729 GTTCAAGGGCTGTGAGACCCTGCGCCCTGGGGGAGAAGGGCCCCGTTAAGCAGAGAGCAA 788

Qy    2307 CA-CCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACG-CTGACAACA 2364
           || ||| ||||||||||||||||||||||||||||||||||||||||||| || |||||||||
Db     789 CACCCTTCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGGCGCCTGACAACA 848

Qy    2365 ACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCA 2424
           |||||||||||||||||||||||||||||||| |||||| |||||  |||||| |||| ||
Db     849 ACTGCCTAGGCACTGAGGTAGCTTAAACTCTA-GCACAGCCCGGGCTTGCGGGGCAGCCA 907

Qy    2425 CCTGGCCATGCTGGCTGGGCGGCCCA 2450
           |||| ||||||||  |||||||||||
Db     908 CCTGCCCATGCTGTGTGGGCGGCCCA 933


RESULT 13
CB243787/c
LOCUS       CB243787                797 bp    mRNA     linear    EST 12-FEB-2003
DEFINITION  UI-CF-FN0-agg-a-05-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
            UI-CF-FN0-agg-a-05-0-UI 3', mRNA sequence.
ACCESSION   CB243787
VERSION     CB243787.1  GI:28365431
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

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FEATURES              Location/Qualifiers
     source           1. .797
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-CF-FN0-agg-a-05-0-UI"
                      /tissue_type="Human Lung Epithelial cells"
                      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                      /clone_lib="UI-CF-FN0"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      UI-CF-FN0 is a subtracted cDNA library derived from two
                      normalized Human lung epithelial cell libraries (EN1 and
                      DU1) The library was subtracted according to according to
                      Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                      1996. For additional information, contact:
                      bento-soares@uiowa.edu
                      TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                      6hr to LPS 24h
                      TAG_LIB=UI-CF-FN0
                      TAG_SEQ=CTGCTCAGGT"
ORIGIN
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Query Match   24.8%;   Score 779.8; DB 14; Length 797;
Best Local Similarity 99.4%;   Pred. No. 7.3e-179;
Matches 781; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

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Qy     2358 GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417
            |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||
Db      797 GACAACAACTGCNTAGGCACTGAGGTAGCTTAAACTNTAGGCACAGGCCGGGGCTGCGGT 738

Qy     2418 GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA 2477
            ||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      737 GCAGGCACCCGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGANTAGGATGACAGCA 678

Qy     2478 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 2537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      677 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 618

Qy     2538 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 2597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      617 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 558

Qy     2598 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 2657
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      557 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 498
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Qy    2658 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 2717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 438

Qy    2718 AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA 2777
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     437 AAGAGACCCTAAAAAACCTGCCTGTCCTAGGACCCTATGGTAATGAACACCAAACATCTA 378

Qy    2778 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 2837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 318

Qy    2838 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 2897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 258

Qy    2898 GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT 2957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT 198

Qy    2958 TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC 3017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC 138

Qy    3018 TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTT 3077
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     137 TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTT 78

Qy    3078 TGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA 3137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 TGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA 18

Qy    3138 AAAAAA 3143
           ||||||
Db      17 AAAAAA 12
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RESULT 14
BX112994

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LOCUS          BX112994                 801 bp    mRNA    linear    EST 07-FEB-2003
DEFINITION     BX112994 Soares placenta Nb2HP Homo sapiens cDNA clone
               IMAGp998F02225 ; IMAGE:147841, mRNA sequence.
ACCESSION      BX112994
VERSION        BX112994.1  GI:27837970
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 801)
  AUTHORS      Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
               Radelof,U., Schneider,D. and Korn,B.
  TITLE        Human UnigeneSet - RZPD3
  JOURNAL      Unpublished (2003)
  COMMENT      Contact: Ina Rolfs
               RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
               Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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FEATURES              Location/Qualifiers
      source          1. .801
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGp998F02225 ; IMAGE:147841"
                      /sex="Female"
                      /dev_stage="placenta obtained at birth (full term)"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares placenta Nb2HP"
                      /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo.   "
ORIGIN
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  Query Match            24.7%;   Score 775;  DB 13;   Length 801;
  Best Local Similarity  99.4%;   Pred. No. 1.1e-177;
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Qy     2086 TGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACT 2145
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Db        1 TGAAGGTCCCGTTGACC-GGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACT 59

Qy     2146 GGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCA 2205
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Db       60 GGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCA 119

Qy     2206 TCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGA 2265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      120 TCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGA 179

Qy     2266 CCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG 2325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      180 CCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG 239

Qy     2326 AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAG 2385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAG 299
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Qy    2386 CTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCG 2445
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Db     300 CTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCG 359

Qy    2446 GCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAGACCACCTTTCTCCCCTGAG 2505
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Db     360 GCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAGACCACCTTTCTCCCCTGAG 419

Qy    2506 AGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTG 2565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 AGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTG 479

Qy    2566 CCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC 2625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC 539

Qy    2626 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCC 2685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCC 599

Qy    2686 ATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCC 2745
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Db     600 ATTCCAGGGACCCTCCAGAAACACAGTGNTTCAAGAGACCCTAAAAAACCTGCCTGTCCC 659

Qy    2746 AGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCT 2805
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Db     660 AGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCT 719

Qy    2806 GGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATG 2865
           ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     720 GGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTNCCAGGGTCATG 779

Qy    2866 CA-GGGATCTGCTCCCTCCTGC 2886
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Db     780 CAGGGGATCTGCTCCCTNCTGC 801
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RESULT 15
BQ883972

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LOCUS       BQ883972                 912 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8616305 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302388
            5', mRNA sequence.
ACCESSION   BQ883972
VERSION     BQ883972.1  GI:22275980
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2519 row: m column: 13
High quality sequence stop: 601.

FEATURES   Location/Qualifiers
     source   1. .912
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                        /mol_type="mRNA"
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                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH_MGC_113"
                        /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                        EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                        into EcoRI/XhoI sites using the following 5' adaptor:
                        GGCACGAG(G). Library constructed by Ling Hong in the
                        laboratory of Gerald M. Rubin (University of California,
                        Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                        Superscript II RT (Life Technologies). Note: this is a
                        NIH_MGC Library."
ORIGIN

   Query Match   24.5%; Score 769.8; DB 13; Length 912;
   Best Local Similarity   96.7%; Pred. No. 2.2e-176;
   Matches 840; Conservative   0; Mismatches 22; Indels   7; Gaps   5;

Qy   1315 GGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCC 1374
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1 GGACGCCCCTGCTGGTGAAATCTGGCGTGGAG-ATACACGGCTTGCAGTGGAGACAGCCC 59

Qy   1375 AGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCC 1434
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 AGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCC 119

Qy   1435 ACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCC 1494
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 ACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCC 179

Qy   1495 CTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAG 1554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 CTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAG 239

Qy   1555 GCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTG 1614
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Db   240 GCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTG 299

Qy   1615 TGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTT 1674
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Qy   1675 GCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAG 1734
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Db   360 GCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAG 419

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Qy   1735 AGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAA 1794
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Db    420 AGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAA 479

Qy   1795 TCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGT 1854
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Db    480 TCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGT 539

Qy   1855 CAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCA 1914
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Db    540 CAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCA 599

Qy   1915 CTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGT 1974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGT 659

Qy   1975 GCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGG 2034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGG 719

Qy   2035 ACCAGACCCT-GGCCCTGGATCCTGAACTGGCAGGCAT-CCCCCGGGAGCATGTGAAGGT 2092
          | |||||||| |||||||||||||||||||| |||||| ||||||||||||||||| ||
Db    720 AACAGACCCTGGGCCCTGGATCCTGAACTGGGAGGCATCCCCCCGGGAGCATGTGAAAGT 779

Qy   2093 CCCGTTGACCAGGGTCAGTGG--TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCC 2150
          |||||||||||||||| |||   ||| | ||| | |||||| || |||||||||||||
Db    780 CCCGTTGACCAGGGTCCATGGGTGGGGCCGGCCTGGCTTGCCCAACAATCCTACTGGCCC 839

Qy   2151 C--ACTTTGTCACTGTCACTGTCCTCTTT 2177
          |     || | |||||| |||| || | ||
Db    840 CCACTTTGGCCACTGTTACTGGCCCCCTT 868
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Search completed: May 13, 2004, 15:34:10
Job time : 7730 secs

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                        GenCore version 5.1.6
              Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          May 13, 2004, 07:58:58 ; Search time 12062 Seconds
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Title:           US-10-015-391A-276
Perfect score:   3143
Sequence:        1 gggctgaggcactgagagac..........aaatataaggcttaaaaaaa 3143


Scoring table:   IDENTITY_NUC
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Searched:        3470272 seqs, 21671516995 residues


Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3143	100.0	3143	6	AX697208	AX697208 Sequence
2	3143	100.0	3143	9	AY358531	AY358531 Homo sapi
3	3068.4	97.6	3257	9	BC020974	BC020974 Homo sapi
4	3041.4	96.8	3252	9	AB029394	AB029394 Homo sapi
5	3035.8	96.6	3191	6	BD249136	BD249136 27 human
6	2927.6	93.1	3151	9	HSM807023	BX640891 Homo sapi
7	2682.2	85.3	2981	6	AX746794	AX746794 Sequence
8	2682.2	85.3	2981	9	AK091127	AK091127 Homo sapi
9	2476.4	78.8	2768	6	AX512887	AX512887 Sequence
c 10	2281	72.6	2281	6	AX528271	AX528271 Sequence
11	2228.4	70.9	2271	6	AX528269	AX528269 Sequence
12	1834.8	58.4	1838	6	AX879068	AX879068 Sequence
13	1834.8	58.4	1838	6	BD157628	BD157628 Primer fo
14	1834.8	58.4	1838	9	AK022349	AK022349 Homo sapi
15	1760	56.0	3159	10	BC025800	BC025800 Mus muscu
16	1727.6	55.0	3046	10	MMRNASEMB	X85991 M.musculus
17	1340	42.6	164168	9	AL135927	AL135927 Human DNA
c 18	1340	42.6	164179	9	AC007227	AC007227 Homo sapi
19	696.6	22.2	775	6	AX866805	AX866805 Sequence
20	696.6	22.2	775	6	BD146867	BD146867 Primer fo
c 21	498	15.8	567	6	AX872305	AX872305 Sequence
c 22	498	15.8	567	6	BD152367	BD152367 Primer fo
23	494	15.7	1223	6	AX704742	AX704742 Sequence
24	486.6	15.5	184850	2	AC102388	AC102388 Mus muscu
25	486.6	15.5	249206	2	AC145168	AC145168 Mus muscu
26	470	15.0	988	6	AX430331	AX430331 Sequence
27	439.6	14.0	230635	2	AC128319	AC128319 Rattus no
28	439.6	14.0	246036	2	AC097816	AC097816 Rattus no
29	439.6	14.0	289877	2	AC119762	AC119762 Rattus no
30	327	10.4	2405	6	AX879101	AX879101 Sequence
31	327	10.4	2405	6	BD157650	BD157650 Primer fo
32	327	10.4	2405	9	AK022416	AK022416 Homo sapi
33	280.4	8.9	106784	2	AC136250	AC136250 Rattus no

34	263.6	8.4	3766	6	BD171175	BD171175 Novel gen
35	263.6	8.4	3766	6	BD183514	BD183514 Novel gen
36	263.6	8.4	3766	9	AB051532	AB051532 Homo sapi
37	263.6	8.4	3781	6	AX376386	AX376386 Sequence
38	263.6	8.4	3781	6	AX697184	AX697184 Sequence
39	263.6	8.4	3781	9	AY358392	AY358392 Homo sapi
40	263.6	8.4	3807	9	AY445887	AY445887 Homo sapi
41	251.6	8.0	3528	9	AK026108	AK026108 Homo sapi
42	246.6	7.8	2390	6	AX418422	AX418422 Sequence
43	237.8	7.6	3293	6	AX174731	AX174731 Sequence
44	236.6	7.5	2155	6	AX060303	AX060303 Sequence
45	236.6	7.5	2156	6	AX060313	AX060313 Sequence

ALIGNMENTS

RESULT 1
AX697208
LOCUS   AX697208   3143 bp   DNA   linear   PAT 02-APR-2003
DEFINITION   Sequence 276 from Patent WO0078961.
ACCESSION   AX697208
VERSION   AX697208.1 GI:29498147
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
               Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
               Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
               Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
  TITLE   Secreted and transmembrane polypeptides and nucleic acids encoding
               the same
  JOURNAL   Patent: WO 0078961-A 276 28-DEC-2000;
               Genentech Inc. (US)
FEATURES   Location/Qualifiers
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ORIGIN

     Query Match   100.0%; Score 3143; DB 6; Length 3143;
     Best Local Similarity 100.0%; Pred. No. 0;
     Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

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Db   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy   181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Db   181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
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Db   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
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ORIGIN

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Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
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Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy      3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT  3120
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Qy      3121  TAAAAATATAAGGCTTAAAAAAA  3143
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RESULT 3
BC020974
LOCUS          BC020974                3257 bp    mRNA      linear    PRI 03-OCT-2003
DEFINITION     Homo sapiens hypothetical protein FLJ12287 similar to semaphorins,
               mRNA (cDNA clone MGC:9542 IMAGE:3847802), complete cds.
ACCESSION      BC020974
VERSION        BC020974.1  GI:18088092
KEYWORDS       MGC.
SOURCE         Homo sapiens (human)
   ORGANISM    Homo sapiens
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 3257)
   AUTHORS     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
               Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
               Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
               Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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               Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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               Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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               Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
               Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
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                    Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                    Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
    TITLE   Generation and initial analysis of more than 15,000 full-length
                    human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2   (bases 1 to 3257)
  AUTHORS   Strausberg,R.
    TITLE   Direct Submission
  JOURNAL   Submitted (03-JAN-2002) National Institutes of Health, Mammalian
                    Gene Collection (MGC), Cancer Genomics Office, National Cancer
                    Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                    USA
   REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT   Contact: MGC help desk
                    Email: cgapbs-r@mail.nih.gov
                    Tissue Procurement: ATCC
                    cDNA Library Preparation: Life Technologies, Inc.
                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                    DNA Sequencing by: Sequencing Group at the Stanford Human Genome
                    Center, Stanford University School of Medicine, Stanford, CA   94305
                    Web site: http://www-shgc.stanford.edu
                    Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                    Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                    R. M.

                    Clone distribution: MGC clone distribution information can be found
                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                    Series: IRAK Plate: 20 Row: i Column: 24
                    This clone was selected for full length sequencing because it
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Db   2027 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGG 2086

Qy   1994 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2053
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Qy   2054 TCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG 2113
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Qy   2114 TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT 2173
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Qy   2174 CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
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RESULT 4
AB029394

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LOCUS       AB029394                3252 bp    mRNA    linear   PRI 06-JAN-2001
DEFINITION  Homo sapiens mRNA for SEMB, complete cds.
ACCESSION   AB029394
VERSION     AB029394.1  GI:12248381
KEYWORDS    SEMB.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 3252)
  AUTHORS   Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
            Miyajima,N. and Saito,T.
  TITLE     Human semaphorin B
  JOURNAL   Published Only in DataBase (2001)
REFERENCE   2  (bases 1 to 3252)
  AUTHORS   Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
            Miyajima,N. and Saito,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-1999) Toshiyuki Saito, National Institute of
            Radiological Sciences, Genome Research Group; Inage-ku Anagawa
            4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp,
            Tel:81-43-201-3135, Fax:81-43-251-9818)
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                     LLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVL
                     KTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGE
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KECRTSASDVDADNNCLGTEVA"

ORIGIN

Query Match   96.8%;   Score 3041.4;   DB 9;   Length 3252;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 3074; Conservative   0; Mismatches   16; Indels   3; Gaps   2;

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Qy      48 GAAACGCAGCGGCATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATG 107
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Db     152 GAAAGTGCCCGGGTGCCTGTTTCCCCAGACCTCCCTGGTGACAGTCTGTGGCTGAGCATG 211

Qy     108 GCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTG 167
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Qy     708 CTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGAC 767
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Qy     2625 CCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGC 2684
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Db     2732 CCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGC 2791

Qy     2685 CATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCC 2744
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Qy     2745 CAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCC 2804
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Db     2852 CAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCC 2911

Qy     2805 TGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCAT 2864
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Db     2912 TGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCAT 2971

Qy     2865 GCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGT 2924
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Qy     3045 CCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAG 3104
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RESULT 5
BD249136
LOCUS   BD249136   3191 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION 27 human secreted proteins.
ACCESSION   BD249136
VERSION   BD249136.1 GI:33058906
KEYWORDS   JP 2002538841-A/10.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3191)

COMMENT   OS   Homo sapiens (human)
           PN   JP 2002538841-A/10
           PD   19-NOV-2002
           PF   16-MAR-2000 JP 2000605787
           PR   18-MAR-1999 US   60/125055
           PI   STEVEN M RUBEN,JIAN NI,REINHARD EBNER,CRAIG
           A ROSEN,YANGGU SHI,
           PI   CHARLES BIRSE,KIMBERLY FLORENCE,GEORGE KOMATSOULIS,DAVID W PI
             LAFLEUR,
           PI   PAUL A MOORE,HENRIK S OLSEN,PAUL E YOUNG
           PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P9/00,A61P17/00,
           PC   A61P19/02,
           PC   A61P25/02,A61P25/16,A61P25/18,A61P25/22,A61P25/24,A61P25/28,
           PC   A61P27/02,
           PC   A61P29/00,A61P29/00,A61P31/04,A61P31/12,A61P35/00,A61P37/00,
           PC   A61P43/00,
           PC   C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
           ,C12P21/02,C12Q1/02,
           PC   C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,C12N15/00,
           PC   C12N5/00,
           PC   A61K37/02
           CC   n equals a,t,g, or c
           CC   n equals a,t,g, or c
           CC   n equals a,t,g, or c
           CC   n equals a,t,g, or c
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ORIGIN

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Qy   103 GCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCC 162
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Qy   223 CCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGG 282
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Db      198 CCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGG 257

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Db      258 GCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGG 317

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Db      318 CTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACA 377

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Db      378 TGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCA 437

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Db      438 ATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCT 497

Qy      523 ACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCT 582
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Qy      583 ACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACC 642
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Db      618 CCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACA 677

Qy      703 ACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGA 762
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 ACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGA 737

Qy      763 CCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGA 822
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      738 CCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGA 797

Qy      823 CCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGC 882
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Db      798 CCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGC 857

Qy      883 TCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGC 942
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Db      858 TCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGC 917

Qy      943 AGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGC 1002
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Db      918 AGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGC 977

Qy     1003 CCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACA 1062
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      978 CCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACA 1037

Qy     1063 TCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTG 1122
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1038 TCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTG 1097
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Qy    1123 CCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG 1182
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Db    1098 CCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG 1157

Qy    1183 AAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCT 1242
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Qy    1243 CAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATG 1302
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Qy    1363 TGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCA 1422
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Qy    1423 CAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGA 1482
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Qy    1483 TTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTG 1542
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Qy    1543 CAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCT 1602
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Qy    1603 ATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGT 1662
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Qy    1663 CCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGC 1722
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Qy    1783 GCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCT 1842
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Qy    1903 AAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGG 1962
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Db    1878 AAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGG 1937
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Qy    1963 GTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGG 2022
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RESULT 6
HSM807023
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DEFINITION Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248);
            complete cds.
ACCESSION   BX640891
VERSION   BX640891.1 GI:34365195
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3151)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
            Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE   Direct Submission
  JOURNAL   Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
  COMMENT   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project. This clone
            (DKFZp686D04248) is available at the RZPD in Berlin. Please contact
            the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
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                     /mol_type="mRNA"
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ORIGIN

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Qy        202 GAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCAC 261
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Db        200 GTGGCTGAGCATGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCAC 259

Qy        262 TTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 TTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATG 319

Qy        322 GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG 381
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Db        320 GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG 379

Qy        382 GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAAT 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAAT 439

Qy        442 GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTT 501
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Qy     502  CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT  561
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Qy     562  TCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA  621
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Db     560  TCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA  619

Qy     622  AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC  681
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Qy     682  TCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG  741
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Qy     742  GATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCT  801
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Qy     802  TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG  861
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Db     800  TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG  859

Qy     862  AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG  921
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Db     860  AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG  919

Qy     922  TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCT  981
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Db     920  TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCT  979

Qy     982  GCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCG  1041
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Db     980  GCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCG  1039

Qy    1042  ATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGA  1101
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Db    1040  ATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGA  1099

Qy    1102  CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA  1161
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Qy    1162  AATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA  1221
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Db    1160  AATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA  1219

Qy    1222  ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGA  1281
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Db    1220  ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGA  1279

Qy    1282  AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG  1341
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Db    1280  AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG  1339
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Qy    1342 TGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG 1401
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Db    1340 TGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG 1399

Qy    1402 TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA 1461
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Db    1400 TCATGTACCTGGGAACCACCCCAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA 1459

Qy    1462 GTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGC 1521
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Db    1460 GTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGC 1519

Qy    1522 AGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGC 1581
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Qy    1582 CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCC 1641
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Qy    1642 ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACT 1701
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Qy    1882 ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA 1941
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Qy    1942 TAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCAT 2001
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Qy    2002 ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC 2061
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Db    2000 ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC 2059

Qy    2062 TGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG 2121
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Db    2060 TGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG 2119

Qy    2122 CCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCT 2181
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Db    2120 CCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCT 2179

Qy    2182 TAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC 2241
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Qy   2242 GGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG 2301
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Db   2240 GGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG 2299

Qy   2302 AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA 2361
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Db    3020 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3079

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Db    3080 ATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3139

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RESULT 7
AX746794
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LOCUS       AX746794                2981 bp    mRNA    linear   PAT 20-JUN-2003
DEFINITION  Sequence 319 from Patent EP1308459.
ACCESSION   AX746794
VERSION     AX746794.1  GI:32131182
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1308459-A 319 07-MAY-2003;
            Helix Research Institute (JP) ; Research Association for
            Biotechnology (JP)
FEATURES             Location/Qualifiers
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ORIGIN
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Qy    242 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 301
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Db    186 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 245

Qy    302 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    306 CTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAG 365

Qy    422 TGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAA 481
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Qy    482  CTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGC  541

Db    412  ------------------------------------------------------------  411


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Db    412  -----------------------GAACTTCAAGATTCCTACCTGTTGCCCATCTCGGA  446


Qy    602  GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGC  661
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Db    447  GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGC  506


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Qy    722  CATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTG  781
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Db    567  CATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTG  626


Qy    782  GCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTT  841
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Qy    902  TAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTT  961
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Qy    1022 CGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTC  1081
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Qy    1262 TAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCC  1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1107 TAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCC  1166
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Qy    1322 CCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCT 1381
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Qy    1442 TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCC 1501
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Db    1287 TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCC 1346

Qy    1502 TGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTC 1561
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Qy    1562 AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG 1621
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Db    1407 AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG 1466

Qy    1622 TGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCT 1681
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Qy    1682 GTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC 1741
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Db    1527 GTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC 1586

Qy    1742 ATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAA 1801
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1862 GGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTA 1921
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Db    1707 GGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTA 1766

Qy    1922 CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGC 1981
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1767 CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGC 1826

Qy    1982 AACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGAC 2041
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    1827 AACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGGCAGCCAGGACCAGAC 1886

Qy    2042 CCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGAC 2101
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Qy    2102 CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC 2161
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Db    1947 CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC 2006

Qy    2162 TGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCC 2221
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Qy    2222  ATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGA  2281
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Db    2067  ATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGA  2126

Qy    2282  GAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC  2341
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Qy    2342  CAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC  2401
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Qy    2402  AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCT  2461
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Db    2247  AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCT  2306

Qy    2462  GACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACT  2521
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Db    2307  GACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACT  2366

Qy    2522  CTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACT  2581
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2367  CTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACT  2426

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Qy    2702  AGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAAT  2761
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Qy    2762  GAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGA  2821
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Db    2667  AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT  2726

Qy    2882  CCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGAC  2941
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Qy    2942  CACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGC  3001
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Db    2787  CACCTTTCTTCTTGCTTCAGTTGGGGCAGACTTTGATCCCTTCTGCCCTGGCAGAATGGC  2846

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              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db     2847 AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCT 2906

Qy     3062 CCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTATT 3121
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Db     2907 CCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTATT 2966

Qy     3122 AAAAATATAAGGCTT 3136
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Db     2967 AAAAATATAAGGCTT 2981
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RESULT 8
AK091127
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LOCUS       AK091127                2981 bp    mRNA    linear    PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ33808 fis, clone CTONG2001749, highly similar
            to SEMAPHORIN 4A PRECURSOR.
ACCESSION   AK091127
VERSION     AK091127.1  GI:21749423
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
            Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
            Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
            Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
            Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
            Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2981)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CTONG2001749"
                     /tissue_type="tongue, tumor tissue"
                     /clone_lib="CTONG2"
                     /note="cloning vector: pME18SFL3"
ORIGIN
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Query Match              85.3%;   Score 2682.2;   DB 9;   Length 2981;
Best Local Similarity    96.5%;   Pred. No. 0;
Matches 2793;   Conservative    0;   Mismatches    3;   Indels   99;   Gaps    1;

Qy     242 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 245

Qy     302 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 305

Qy     362 CTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAG 421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     306 CTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAG 365

Qy     422 TGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAA 481
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     366 TGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAG-------------- 411

Qy     482 CTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGC 541

Db     412 ------------------------------------------------------------ 411

Qy     542 CTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGA 601
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Db     412 --------------------------GAACTTCAAGATTCCTACCTGTTGCCCATCTCGGA 446

Qy     602 GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGC 661
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Db     447 GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGC 506

Qy     662 TGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCC 721
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     507 TGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCC 566

Qy     722 CATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTG 781
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Qy     782 GCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTT 841
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Db     627 GCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTT 686

Qy     842 CTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGC 901
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     687 CTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGC 746

Qy     902 TAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTT 961
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     747 TAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTT 806

Qy     962 CCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCA 1021
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     807 CCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCA 866
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Qy   1022  CGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTC  1081
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Db    927  CCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACAT   986

Qy   1142  TGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTAC  1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    987  TGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTAC  1046

Qy   1202  TTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGA  1261
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Db   1047  TTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGA  1106

Qy   1262  TAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCC  1321
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Db   1107  TAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCC  1166

Qy   1322  CCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCT  1381
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Db   1287  TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCC  1346

Qy   1502  TGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTC  1561
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Db   1347  TGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTC  1406

Qy   1562  AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG  1621
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Db   1407  AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG  1466

Qy   1622  TGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCT  1681
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Qy  2102 CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC 2161
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Qy  2282 GAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC 2341
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Db  2127 GAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC 2186

Qy  2342 CAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC 2401
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  2187 CAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC 2246

Qy  2402 AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCT 2461
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Db  2247 AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCT 2306

Qy  2462 GACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACT 2521
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  2307 GACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACT 2366

Qy  2522 CTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACT 2581
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  2367 CTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACT 2426

Qy  2582 CCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCT 2641
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Db  2427 CCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCT 2486

Qy  2642 ACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCC 2701
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Db  2487 ACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCC 2546

Qy  2702 AGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAAT 2761
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Db     2547 AGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAAT 2606

Qy     2762 GAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGA 2821
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Db     2607 GAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGA 2666

Qy     2822 AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT 2881
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Db     2667 AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT 2726

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Qy     2942 CACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGC 3001
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Qy     3002 AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCT 3061
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Db     2847 AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCT 2906

Qy     3062 CCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATT 3121
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Db     2907 CCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATT 2966

Qy     3122 AAAAATATAAGGCTT 3136
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RESULT 9
AX512887
LOCUS   AX512887   2768 bp   DNA   linear   PAT 03-OCT-2002
DEFINITION Sequence 35 from Patent WO02062841.
ACCESSION   AX512887
VERSION   AX512887.1 GI:23504046
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,T.Y., Yue,H., Gandhi,A.R., Yao,M.G., Warren,B.A., Ding,L.,
            Duggan,B.M., Xu,Y., Yang,J., Thangavelu,K., Lal,P.G.,
            Honchell,C.D., Walia,N.K., Lee,S., Lee,E.A., Richardson,T.W.,
            Baughn,M.R. and Elliott,V.S.
  TITLE   Secreted proteins
  JOURNAL   Patent: WO 02062841-A 35 15-AUG-2002;
            Incyte Genomics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1. .2768
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                     /note="Incyte ID No: 7487507CB1"
ORIGIN

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Query Match          78.8%;   Score 2476.4;   DB 6;   Length 2768;
Best Local Similarity  96.5%;  Pred. No. 0;
Matches 2580;  Conservative  0;  Mismatches  1;  Indels  93;  Gaps  1;

Qy      74 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCC 133
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCC 228

Qy     134 CTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGAC 193
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 CTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGAC 288

Qy     194 CGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACG 253
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 CGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACG 348

Qy     254 TAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAG 313
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 TAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAG 408

Qy     314 TGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCA 373
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 TGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCA 468

Qy     374 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAA 433
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAA 528

Qy     434 GAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGT 493
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     529 GAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGT 588

Qy     494 CCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGC 553
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Db     589 CCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGC 648

Qy     554 TTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCAT 613
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     649 TTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCAT 708

Qy     614 GGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGA 673
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     709 GGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGA 768

Qy     674 TGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCG 733
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     769 TGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCG 828

Qy     734 CACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGA 793
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     829 CACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGA 888

Qy     794 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 853
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     889 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 948
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Qy    854 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA 913
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA 1008

Qy    914 GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCA 973
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Db   1009 GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCA 1068

Qy    974 GCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCT 1033
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 GCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCT 1128

Qy   1034 CCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGT 1093
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 CCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGT 1188

Qy   1094 TGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTT 1153
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTT 1248

Qy   1154 TAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCC 1213
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Db   1249 TAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCC 1308

Qy   1214 TGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGAC 1273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 TGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGAC 1368

Qy   1274 CTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAA 1333
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 CTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAA 1428

Qy   1334 ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG 1393
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG 1488

Qy   1394 CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGG 1453
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Db   1489 CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT--------- 1539

Qy   1454 GGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCG 1513

Db   1540 ------------------------------------------------------------ 1539

Qy   1514 CAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG 1573
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Db   1540 ----------------------GGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG 1575

Qy   1574 GAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCG 1633
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Db   1576 GAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCG 1635

Qy   1634 GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA 1693
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA 1695

Qy   1694 CCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG 1753
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Db    1696 CCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG 1755

Qy    1754 CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGC 1813
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Qy    1814 TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTA 1873
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Db    1816 TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTA 1875

Qy    1874 TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1933
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Db    1876 TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1935

Qy    1934 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGG 1993
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Db    1936 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGG 1995

Qy    1994 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2053
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Db    1996 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2055

Qy    2054 TCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG 2113
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Db    2056 TCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG 2115

Qy    2114 TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT 2173
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Qy    2174 CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
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Qy    2234 CCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTT 2293
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Qy    2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2353
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Db    2296 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2355

Qy    2354 CGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG 2413
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Db    2356 CGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG 2415

Qy    2414 CGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGAC 2473
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Db    2416 CGGTGCAGGCACCCGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGAC 2475

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Qy    2534 TGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAA 2593
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Qy    2654 AAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTG 2713
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Qy    2714 TTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAG 2747
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RESULT 10
AX528271/c

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LOCUS       AX528271                2281 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 9 from Patent WO0206339.
ACCESSION   AX528271
VERSION     AX528271.1  GI:25172573
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K.,
            Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M.,
            Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,
            Shimkets,R.A. and Padigaru,M.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0206339-A 9 24-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN
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  Matches 2281;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy     125 CCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCC 184
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Db    2281 CCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCC 2222

Qy     185 GACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGG 244
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Db    2221 GACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGG 2162

Qy     245 GGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCT 304
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Db    2161 GGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCT 2102
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Qy    305 GCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTT 364
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTT 2042

Qy    365 GGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGA 424
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGA 1982

Qy    425 CAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTT 484
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTT 1922

Qy    485 CATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTT 544
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTT 1862

Qy    545 CAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGA 604
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Db   1861 CAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGA 1802

Qy    605 CAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGT 664
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGT 1742

Qy    665 CTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCAT 724
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Db   1741 CTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCAT 1682

Qy    725 CCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCT 784
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Db   1681 CCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCT 1622

Qy    785 GCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTT 844
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Db   1621 GCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTT 1562

Qy    845 CGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAG 904
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Db   1561 CGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAG 1502

Qy    905 AGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCT 964
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Qy    965 GAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGC 1024
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Db   1441 GAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGC 1382

Qy   1025 GGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCA 1084
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Qy   1085 GTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGA 1144
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Qy   1145 ACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTA 1204
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Db    1261 ACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTA 1202

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Qy    1445 GGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGA 1504
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Qy    1505 ACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGG 1564
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Db     901 ACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGG 842

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Db     481 TGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAAC 422

Qy    1985 TGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCT 2044
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Db      421  TGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCT  362

Qy     2045  GGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAG  2104
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Db      361  GGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAG  302

Qy     2105  GGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGT  2164
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Db      301  GGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGT  242

Qy     2165  CACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATT  2224
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Db      241  CACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATT  182

Qy     2225  GAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAA  2284
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Db      181  GAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAA  122

Qy     2285  GGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAG  2344
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Db      121  GGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAG  62

Qy     2345  TGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG  2404
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DEFINITION  Sequence 7 from Patent WO0206339.
ACCESSION   AX528269
VERSION     AX528269.1  GI:25172572
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K.,
            Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M.,
            Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,
            Shimkets,R.A. and Padigaru,M.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0206339-A 7 24-JAN-2002;
            Curagen Corporation (US)
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ORIGIN
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Best Local Similarity  98.9%;   Pred. No. 0;
Matches 2260;  Conservative    0;  Mismatches   11;  Indels   15;  Gaps    1;

Qy     105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy     165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 224
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 120

Qy     225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy     285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy     345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
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Db     241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 300

Qy     405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy     465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Db     361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

Qy     525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
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Db     421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 480

Qy     585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
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Db     481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 540

Qy     645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 600

Qy     705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
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Db     601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 660

Qy     765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
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Qy     825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884
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Db     721 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 780

Qy     885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944
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Db      781  CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG  840

Qy      945  AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC  1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC  900

Qy     1005  TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC  1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC  960

Qy     1065  TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC  1124
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Db      961  TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC  1020

Qy     1125  TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA  1184
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Db     1021  TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA  1080

Qy     1185  ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA  1244
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Db     1081  ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA  1140

Qy     1245  GTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG  1304
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Db     1141  GTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG  1200

Qy     1305  CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG  1364
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Db     1201  CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG  1260

Qy     1365  GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA  1424
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Db     1321  GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT  1380

Qy     1485  CAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA  1544
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Qy     1605  GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC  1664
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Qy     1665  CGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG  1724
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Db    1606 GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC 1665

Qy    1785 CGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC 1844
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Qy    1965 CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG 2024
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Qy    2265 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2324
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Qy    2385 GCTTAA 2390
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RESULT 12
AX879068
LOCUS        AX879068                1838 bp    DNA        linear    PAT 17-DEC-2003
DEFINITION   Sequence 13973 from Patent EP1074617.
ACCESSION    AX879068
VERSION      AX879068.1  GI:40033804
KEYWORDS     .
SOURCE       Homo sapiens (human)
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Qy     1419 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 1478
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Qy     1479 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 1538
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DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD157628
VERSION   BD157628.1 GI:27863386
KEYWORDS   JP 2002191363-A/12471.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1838)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE   Primer for synthesizing full-length cDNA and use thereof
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Qy   1299 GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT 1358
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DEFINITION Homo sapiens cDNA FLJ12287 fis, clone MAMMA1001771, moderately
            similar to M.musculus mRNA for semaphorin B.
ACCESSION   AK022349
VERSION   AK022349.1 GI:10433727
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
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Qy    1299 GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT 1358
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Db       1 GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT 60

Qy    1359 GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 1418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 120

Qy    1419 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 1478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1479 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 1538
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Qy    1539 GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT 1598
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Qy    1599 GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT 1658
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Qy    1659 GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATG 1718
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Qy    2019 TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG 2078
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Qy    2139 TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC 2198
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Qy    2199 CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGC 2258
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Qy    2259 TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT 2318
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Qy    2319 CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT 2378
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Qy     2439  CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC  2498
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     RESULT 15
     BC025800
     LOCUS        BC025800              3159 bp    mRNA    linear    ROD 12-NOV-2003
     DEFINITION   Mus musculus sema domain, immunoglobulin domain (Ig), transmembrane
                  domain (TM) and short cytoplasmic domain, (semaphorin) 4A, mRNA
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                   (cDNA clone MGC:35988 IMAGE:5102015), complete cds.
ACCESSION     BC025800
VERSION       BC025800.1  GI:19387926
KEYWORDS      MGC.
SOURCE        Mus musculus (house mouse)
  ORGANISM    Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1  (bases 1 to 3159)
  AUTHORS     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
              Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
              Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
              Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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              Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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              Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
              Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
              Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
              Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
    TITLE     Generation and initial analysis of more than 15,000 full-length
              human and mouse cDNA sequences
  JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   MEDLINE    22388257
    PUBMED    12477932
REFERENCE     2  (bases 1 to 3159)
  AUTHORS     Strausberg,R.
    TITLE     Direct Submission
  JOURNAL     Submitted (11-MAR-2002) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
   REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT     Contact: MGC help desk
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Jeffrey E. Green, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Genome Sequence Centre,
              BC Cancer Agency, Vancouver, BC, Canada
              info@bcgsc.bc.ca
              Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
              Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
              Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
              Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
              Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
              Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
              Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
              George Yang, Scott Zuyderduyn, Marco Marra.
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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 57 Row: j Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7305468.

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ORIGIN
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Query Match   56.0%; Score 1760; DB 10; Length 3159;

Best Local Similarity   76.7%;   Pred. No. 0;
Matches 2356;   Conservative   0;   Mismatches 620;   Indels   94;   Gaps   13;

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Qy        75 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCC 134
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Db       252 TCTGGGACTGGTGGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGACGGGCAC 311

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Db    1512 GACAGCAGTGCTTATCTCGTGGAGGAGATTCAGCTGAGCCCTGACTCTGAGCCTGTTCGA 1571

Qy    1515 AACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGG 1574
           |||||||||||||||||| ||||||||||||||||| ||||||||||| |||||  |||||
Db    1572 AACCTGCAGCTGGCCCCCGCCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTGG 1631

Qy    1575 AGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGG 1634
           || || ||| | ||||| || ||||||||| ||||||||||||||||||||| ||||| ||
Db    1632 AGAGTTCCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGG 1691

Qy    1635 GACCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAAC 1694
           ||||| |||||||||||||||||||| || || |||  |||| ||||||| | | |
Db    1692 GACCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTCTACC 1751

Qy    1695 CTGAACTCCTGGAAGCAGGACATGGAGCGGGGGGAACCCAGAGTGGGCATGTGCCAGTGGC 1754
           ||  | |||||||||||||||||||||| || || ||||| ||||||| ||| || ||||||
Db    1752 ---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTATGCACCGTGGC 1808
```

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Qy    1755 CCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCT 1814
           ||||||  ||||||||  ||||  ||||||||  |||  |||  |  ||||||||||||||| |
Db    1809 CCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCCTCAACTAATTAAAGAAGTCCTGACA 1868

Qy    1815 GTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTAT 1874
           ||||||||||||||||||||||||| |||||||||||||||||||||| |||||||||| |
Db    1869 GTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCCACCTGTCAGCACTGGCCTCTTACCAC 1928

Qy    1875 TGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTC 1934
           ||||||||||||| |||   | | || ||||||||||| | || ||||||||||||||||||
Db    1929 TGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGGCTCCCTC 1988

Qy    1935 TTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGC 1994
           ||||||  |  |||||||||| || |||||  ||||||||||| |   ||| |||||| |||
Db    1989 TTGCTGCTGCCGCAGGATGGTGTCGGGGGCCTCTACCAGTGTGTGGCGACTGAGAACGGC 2048

Qy    1995 TTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGAT 2054
           |  ||||||||||| |||||||| ||||| ||||||||||||||| |||||||| |||||
Db    2049 TACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCTGGCGCTGGAC 2108

Qy    2055 CCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGT 2114
           |||| |||||| ||| ||| | ||||| |||| |||| ||||||| ||||||||||| | ||
Db    2109 CCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGGC 2168

Qy    2115 GGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTC 2174
           || ||   || ||||||||||||| ||||||||||||||| ||| |||  || || ||||||
Db    2169 GGAGCTTCCATGGCTGCCCAGCGGTCCTACTGGCCCCATTTTCTCATCGTTACCGTCCTC 2228

Qy    2175 TTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTC 2234
           | ||| | |||||| |   |||| |   || ||||||||| | | |||||||| || | | ||
Db    2229 CTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCTG 2288

Qy    2235 CGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTA 2294
           |||||||||||| |||||||||||||||| |||| | | ||| ||| |||||| || |
Db    2289 CGGGCTCGGGGTAAGGTTCAGGGCTGTGGGATGCTGCCCCCCAGGGGAAAGGCTCCACTG 2348

Qy    2295 AGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGAC 2354
           ||||| || || |||||||| ||| ||||||| ||     |||||||||||||||||| || ||
Db    2349 AGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGAT 2408

Qy    2355 GCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCT-- 2412
           || |||||||||  |||| || |  |||| | || ||| ||||||||               ||| |||
Db    2409 GCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCGCAGCTGA 2468

Qy    2413 GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGA 2472
           || | ||| ||  ||||| || ||||| || |  |||      ||
Db    2469 GCAGAGCAAGCCACTGGCCTTGTTGGCTATGC--------------------------- 2500

Qy    2473 CAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTG 2532
              |||    |  | |   ||  |      |   |||| || ||||||    ||  ||||
Db    2501 ---CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGTGTCACCT 2557

Qy    2533 ATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCA 2592
           |   ||| ||| |||                      |||||||| |||||||| |||||  | |
Db    2558 ACAGCACCCAGTAGG------------------TCCTCCCCTGTGGGACTCTCTTCTGCAA 2600
```

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Qy    2593 AGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATT 2652
           || ||| |||                          ||| |||||| | |   ||| |
Db    2601 GCACATTGGGCTGTCT-------------------CCATACCTGTACTTGTGCTGTGACA 2641

Qy    2653 GAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGT 2712
           | |  | |  || ||| | |||    || ||      ||| |  |||||| | |||| |
Db    2642 GGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTCCTGTAACAAACG 2701

Qy    2713 GTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAAC 2772
           || ||    ||   |||          |  |||  || ||||| |  ||| | || |
Db    2702 TGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGACAAAC-CTAAGC 2760

Qy    2773 ATCTAAACAATCATATGCTA-------ACATGCCACTCCTGGAAACTCCACTCT----GA 2821
           ||| | ||| |      ||||        | | ||| |           |||||||     |
Db    2761 ATCCGAGCAAGCTGGGGCTATTCCTGCAAACTCCATCCTGAACGCTGTCACTCTAGAAGC 2820

Qy    2822 AGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           |||||| |||||| |||||| |||||| | | |||| | |||||| |     | | ||| || |||
Db    2821 AGCTGCTGCTTTGAACACCAGCCCACCCTCCTTCCCAAGAGTCTCTATGGAGTTGGCCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           |  || |||| |||||||||| |||        ||| |      |||||| | |||||||||| |
Db    2881 TTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTAA 2937

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGC-AGA 2996
           ||||||| ||||||||||||||| || |||| | | ||    |    ||||||||||| |||
Db    2938 CCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGA 2997

Qy    2997 ATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTC 3056
           ||||  ||  ||||||||||||| || |   |   | |||||||| |   |    |
Db    2998 ATGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCCAGTGTGGCTGACCCTTGACCTCTT- 3056

Qy    3057 CCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTT 3116
           || |||    |  ||||||||||||||||||||||||||||||||||||||||| ||||   ||||||||
Db    3057 -CCTTCCTCCTCCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCACAGACAATTTATTTT 3115

Qy    3117 TTATTAAAAA 3126
           ||||||||||
Db    3116 TTATTAAAAA 3125
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                         GenCore version 5.1.6
                Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          May 13, 2004, 07:57:08 ; Search time 1158 Seconds
                                          (without alignments)
                                          11530.299 Million cell updates/sec


Title:           US-10-015-391A-276
Perfect score:   3143
Sequence:        1 gggctgaggcactgagagac.........aaatataaggcttaaaaaaa 3143


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        3373863 seqs, 2124099041 residues


Total number of hits satisfying chosen parameters:      6747726


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       N_Geneseq_29Jan04:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002s:*
                 7:  geneseqn2003as:*
                 8:  geneseqn2003bs:*
                 9:  geneseqn2003cs:*
                 10:  geneseqn2004s:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                               SUMMARIES
                  %
Result          Query
   No.   Score  Match Length DB   ID                      Description
-------------------------------------------------------------------------------
     1   3143  100.0   3143   3   AAC58392                Aac58392 Human PRO
     2   3143  100.0   3143   8   ACD68436                Acd68436 Novel hum
     3   3143  100.0   3143   8   ACH04538                Ach04538 Human cDN
     4   3143  100.0   3143   8   ACD68082                Acd68082 Novel hum
     5   3143  100.0   3143   9   ADC18145                Adc18145 Human PRO
     6   3143  100.0   3143   9   ADD70791                Add70791 Human cDN
     7   3143  100.0   3143   9   ADD39868                Add39868 Human cDN
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	8	3143	100.0	3143	9	ADD70314	Add70314 Human cDN
	9	3143	100.0	3143	9	ADD38435	Add38435 Human cDN
	10	3143	100.0	3143	9	ADD39391	Add39391 Human cDN
	11	3143	100.0	3143	9	ADD38914	Add38914 Human cDN
	12	3143	100.0	3143	9	ADD40345	Add40345 Human cDN
	13	3143	100.0	3143	9	ADE50566	Ade50566 Human cDN
	14	3143	100.0	3143	9	ADE20178	Ade20178 Human cDN
	15	3143	100.0	3143	9	ADE50089	Ade50089 Human cDN
	16	3143	100.0	3143	9	ADE21647	Ade21647 Human cDN
	17	3131	99.6	3142	3	AAA37100	Aaa37100 Human PRO
	18	3075	97.8	3075	4	AAF54397	Aaf54397 DNA encod
	19	3041.4	96.8	3252	9	ADD67570	Add67570 Human Ly6
	20	3040.8	96.7	3104	5	AAF45125	Aaf45125 Human TAN
	21	3040.8	96.7	3104	7	ABX94103	Abx94103 cDNA enco
	22	3040.8	96.7	3104	7	ACD66780	Acd66780 Secreted
	23	3035.8	96.6	3191	3	AAC69084	Aac69084 Human sec
	24	3029.8	96.4	3042	4	AAK53428	Aak53428 Human pol
	25	3028.2	96.3	3042	7	ABX13628	Abx13628 Human cyt
	26	2860.4	91.0	3146	7	ACC69002	Acc69002 Human neu
	27	2682.2	85.3	2981	9	ADB62165	Adb62165 Human cDN
	28	2476.4	78.8	2768	6	ABS64946	Abs64946 Human cDN
	29	2437	77.5	2745	7	ACC68985	Acc68985 Human neu
	30	2283	72.6	2283	5	AAF45126	Aaf45126 Human TAN
	31	2283	72.6	2283	7	ACD66781	Acd66781 Secreted
c	32	2281	72.6	2281	6	AAD28945	Aad28945 Human MOL
c	33	2281	72.6	2281	9	ADD18199	Add18199 Human mol
	34	2228.4	70.9	2271	6	AAD28944	Aad28944 Human MOL
	35	2228.4	70.9	2271	9	ADD18197	Add18197 Human mol
	36	2104.8	67.0	2238	7	ACC69003	Acc69003 Human neu
	37	1834.8	58.4	1838	4	AAH15636	Aah15636 Human cDN
	38	1727.6	55.0	3046	5	AAF45137	Aaf45137 Murine se
	39	1727.6	55.0	3046	5	AAF45140	Aaf45140 Murine DN
	40	1727.6	55.0	3046	7	ACD26369	Acd26369 Secreted
	41	1727.6	55.0	3046	7	ACD26370	Acd26370 Secreted
c	42	1714.8	54.6	1901	4	AAK53434	Aak53434 Human pol
	43	1015.8	32.3	1674	6	ABK94920	Abk94920 Human nov
	44	925.8	29.5	1730	6	ABS54021	Abs54021 cDNA enco
	45	696.6	22.2	775	4	AAH04875	Aah04875 Human cDN

ALIGNMENTS

RESULT 1
AAC58392
ID   AAC58392 standard; cDNA; 3143 BP.
XX
AC   AAC58392;
XX
DT   29-JAN-2001   (first entry)
XX
DE   Human PRO1317 nucleotide sequence SEQ ID NO:70.
XX
KW   Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW   proliferation; tumourigenesis; identification; cancer; cytostatic;
KW   nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW   immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;

CC   The present invention describes an isolated antibody that binds to one of
CC   the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
CC   PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC   PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC   PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC   PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC   PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC   and prevention of cancer. The antibodies and other anti-tumour compounds
CC   maybe used to treat various conditions, including those characterised by
CC   overexpression and/or activation of the amplified PRO genes. Exemplary
CC   conditions or disorders to be treated with such antibodies and other
CC   compounds include benign or malignant tumours (e.g., renal, liver,
CC   kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC   pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC   glioblastomas, and various head and neck tumours), leukaemias and
CC   lymphoid malignancies, other disorders such as neuronal, glial,
CC   astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC   stromal and blastocoelic disorders, and inflammatory, angiogenic and
CC   immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
CC   hybridisation probes used in the isolation of the human PRO sequences.
CC   AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
CC   polynucleotide and protein sequences given in the exemplification of the

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Qy         1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy        61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy       121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy       181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy       241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy       301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy       361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy       421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy       481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy       541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy       601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy       661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy       721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy      1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy      1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy      1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy      1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy      1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy      1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy      1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy      1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
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Db      1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy      1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy      1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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DT   17-SEP-2003  (first entry)
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RESULT 3
ACH04538
ID   ACH04538 standard; cDNA; 3143 BP.
XX
AC   ACH04538;
XX
DT   01-OCT-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnerary;
KW   cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW   adrenal cortical capillary; endothelial cell growth; wound healing;
KW   stimulated T-lymphocyte proliferation; immune response suppression;
KW   neonatal heart hypertrophy; cardiac insufficiency disorder;
KW   vascular endothelial growth factor; inflammation; mononuclear cell;
KW   eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW   chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW   sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003044841-A1.
XX
PD   06-MAR-2003.
XX
PF   06-DEC-2001; 2001US-00006856.
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  Best Local Similarity  100.0%;  Pred. No. 0;
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RESULT 4
ACD68082
ID   ACD68082 standard; cDNA; 3143 BP.
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AC   ACD68082;
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DT   17-SEP-2003  (first entry)
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DE   Novel human secreted and transmembrane protein PRO1317 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW   tissue typing; chromosome identification; vaccine; gene; ss.
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OS   Homo sapiens.
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PN   US2003073129-A1.
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PD   17-APR-2003.
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PF   04-SEP-2001; 2001US-00946374.
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PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
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DR    WPI; 2003-585292/55.
DR    P-PSDB; ABO33537.
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RESULT 5

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DE    Human PRO polynucleotide #79.
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KW    Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;
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Qy       841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Db       841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy       901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
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Db       901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy       961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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Db       961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy      1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db      1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy      1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
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Qy   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
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Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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RESULT 6
ADD70791

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ID    ADD70791 standard; cDNA; 3143 BP.
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AC    ADD70791;
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DT    15-JAN-2004   (first entry)
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DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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OS    Homo sapiens.
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PN    US2003099625-A1.
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PD    29-MAY-2003.
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XX
PA    (GETH ) GENENTECH INC.
XX
PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
XX
DR    WPI; 2003-874602/81.
DR    P-PSDB; ADD70792.
XX
PT    Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT    PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT    cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
PS    Claim 2; SEQ ID NO 276; 553pp; English.
XX
CC    The invention relates to an isolated PRO polypeptide (secreted or
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    Query Match   100.0%; Score 3143; DB 9; Length 3143;
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    Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
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Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Qy      2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy      2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy      2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy      2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy      2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy      2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db      2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Db      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy      3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy      3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy      3121 TAAAAATATAAGGCTTAAAAAAA 3143
             |||||||||||||||||||||||
Db      3121 TAAAAATATAAGGCTTAAAAAAA 3143
```

RESULT 7
ADD39868
ID   ADD39868 standard; cDNA; 3143 BP.
XX
AC   ADD39868;
XX
DT   15-JAN-2004   (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.

```
XX
OS    Homo sapiens.
XX
PN    US2003083462-A1.
XX
PD    01-MAY-2003.
XX
PF    10-DEC-2001; 2001US-00013913.
XX
PR    05-JAN-1999;    99WO-US000106.
PR    01-SEP-1999;    99WO-US020111.
PR    15-SEP-1999;    99WO-US021194.
PR    30-NOV-1999;    99WO-US028313.
PR    02-DEC-1999;    99WO-US028551.
PR    16-DEC-1999;    99WO-US030095.
PR    05-JAN-2000;  2000WO-US000219.
PR    06-JAN-2000;  2000WO-US000376.
PR    11-FEB-2000;  2000WO-US003565.
PR    18-FEB-2000;  2000WO-US004342.
PR    24-FEB-2000;  2000WO-US005004.
PR    02-MAR-2000;  2000WO-US005841.
PR    15-MAR-2000;  2000WO-US006884.
PR    17-MAY-2000;  2000WO-US013705.
PR    22-MAY-2000;  2000WO-US014042.
PR    30-MAY-2000;  2000WO-US014941.
PR    02-JUN-2000;  2000WO-US015264.
PR    23-AUG-2000;  2000WO-US023522.
PR    24-AUG-2000;  2000WO-US023328.
PR    08-NOV-2000;  2000WO-US030952.
PR    10-NOV-2000;  2000WO-US030873.
PR    01-DEC-2000;  2000WO-US032678.
PR    28-FEB-2001;  2001WO-US006520.
PR    01-MAR-2001;  2001WO-US006666.
PR    01-JUN-2001;  2001WO-US017800.
PR    20-JUN-2001;  2001WO-US019692.
PR    29-JUN-2001;  2001WO-US021066.
PR    09-JUL-2001;  2001WO-US021735.
PR    04-SEP-2001;  2001US-00946374.
XX
PA    (GETH ) GENENTECH INC.
XX
PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
XX
DR    WPI; 2003-755122/71.
DR    P-PSDB; ADD39869.
XX
PT    New secreted and transmembrane PRO polypeptides useful for treating
PT    cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT    hypo-insulinemia, sports injuries and arthritis.
XX
PS    Claim 2; SEQ ID NO 276; 557pp; English.
XX
CC    The invention relates to an isolated PRO polypeptide (secreted or
CC    transmembrane protein) having at least 80% amino acid sequence identity
```

CC   to an amino acid sequence chosen from 123 fully defined sequences as
CC   given in the specification (including their extracellular domains either
CC   or without their associated signal peptides. Also include are the
CC   nucleotide (NA)sequences encoding PRO, a vector comprising the PRO NA, a
CC   host cell comprising the vector, producing PRO, a chimaeric molecule
CC   comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC   PRO antibody. Pro is useful as molecular weight markers for protein
CC   electrophoresis and also for chromosome identification. PRO is also
CC   useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC   probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC   useful for generating transgenic animals or knock-out animals which are
CC   useful in development and screening useful reagents. PRO NA is also
CC   useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC   useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC   polypeptides are useful for suppressing immune response. PRO1246
CC   polypeptide is useful for treating cardiac insufficiency disorders.
CC   PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC   PRO1561 polypeptide are useful for stimulating calcium flux in human
CC   umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC   polypeptides are useful for treating bone and/or cartilage disorders
CC   (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC   polypeptides are useful for treating diabetes in skeletal muscle cells
CC   and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC   treating Berger disease or other nephropathies associated with Schonlein-
CC   Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
CC   disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC   PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC   sequence encodes a PRO protein of the invention.
XX
SQ   Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

     Query Match   100.0%; Score 3143; DB 9; Length 3143;
     Best Local Similarity   100.0%; Pred. No. 0;
     Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db	301	CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG	360

Qy 361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy 421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy 481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy 541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy 601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy 661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy 721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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RESULT 8
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ID   ADD70314 standard; cDNA; 3143 BP.
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AC   ADD70314;
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DT   15-JAN-2004   (first entry)
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DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS   Homo sapiens.
XX
PN   US2003054406-A1.
XX
PD   20-MAR-2003.
XX
PF   06-DEC-2001; 2001US-00006818.
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PR    05-JAN-1999;    99WO-US000106.
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PT   Novel isolated PRO polypeptide useful for tissue typing, modulating
PT   biological activity of cell, as molecular weight markers in protein
PT   electrophoresis, for treating arthritis, tumor.
XX
PS   Claim 2; SEQ ID NO 276; 549pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide (secreted or

    Query Match   100.0%; Score 3143; DB 9; Length 3143;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

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Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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RESULT 9
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ID    ADD38435 standard; cDNA; 3143 BP.
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AC    ADD38435;
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DT    15-JAN-2004   (first entry)
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DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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PR     28-FEB-2001;  2001WO-US006520.
PR     01-MAR-2001;  2001WO-US006666.
PR     01-JUN-2001;  2001WO-US017800.
PR     20-JUN-2001;  2001WO-US019692.
PR     29-JUN-2001;  2001WO-US021066.
PR     09-JUL-2001;  2001WO-US021735.
PR     04-SEP-2001;  2001US-00946374.
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PA     (GETH ) GENENTECH INC.
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PI     Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
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RESULT 10
ADD39391
ID   ADD39391 standard; cDNA; 3143 BP.
XX
AC   ADD39391;
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DT   15-JAN-2004   (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS   Homo sapiens.
XX
PN   US2003096954-A1.
XX
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XX
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RESULT 11
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KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
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PR    16-APR-1999;    99US-0129674P.
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PA    (GETH ) GENENTECH INC.
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PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
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DR    WPI; 2003-765477/72.
DR    P-PSDB; ADD38915.
XX
PT    New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,
PT    PRO1244, PRO1246, useful for treating cancerous tumors, cardiac
PT    insufficiency disorders, wound healing, Crohn's disease, celiac disease.
XX
PS    Claim 2; SEQ ID NO 276; 555pp; English.
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CC    The invention relates to an isolated PRO polypeptide (secreted or
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Query Match              100.0%;  Score 3143;  DB 9;   Length 3143;
Best Local Similarity    100.0%;  Pred. No. 0;
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Db      3121  TAAAAATATAAGGCTTAAAAAAA  3143


RESULT 12
ADD40345
ID    ADD40345 standard; cDNA; 3143 BP.
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AC    ADD40345;
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DT    15-JAN-2004  (first entry)
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DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
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RESULT 13
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DT   29-JAN-2004 (first entry)
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DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
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Db     3121 TAAAAATATAAGGCTTAAAAAAA 3143


RESULT 14
ADE20178
ID     ADE20178 standard; cDNA; 3143 BP.
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AC     ADE20178;
XX
DT     29-JAN-2004   (first entry)
XX
DE     Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW     Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW     immune response; cardiac insufficiency disorder; calcium flux;
KW     umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW     arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW     Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW     dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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OS     Homo sapiens.
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XX
PA    (GETH ) GENENTECH INC.
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PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
XX
DR    WPI; 2003-765493/72.
DR    P-PSDB; ADE20179.
XX
PT    New isolated PRO polypeptide useful for tissue typing, modulating
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PT   biological activity of cell, as molecular weight markers in protein
PT   electrophoresis, for treating arthritis and tumors.
XX
PS   Claim 2; SEQ ID NO 276; 555pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide (secreted or

Query Match   100.0%; Score 3143; DB 9; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT  3120
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RESULT 15
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ID   ADE50089 standard; cDNA; 3143 BP.
XX

AC   ADE50089;
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DT   29-JAN-2004   (first entry)
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DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
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KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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OS   Homo sapiens.
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PN   US2003082626-A1.
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PD   01-MAY-2003.
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PF   06-DEC-2001; 2001US-00006116.
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Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Search completed: May 13, 2004, 10:04:06
Job time : 1169 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:33:13 ; Search time 212 Seconds
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Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.........aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
                    Query
Result   Query
   No.   Score   Match Length DB   ID   Description
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        1   230   7.3   2433   4   US-09-300-958A-24   Sequence 24, Appl
        2   153.4   4.9   4157   4   US-08-556-422A-1   Sequence 1, Appli
        3   126   4.0   3524   4   US-09-077-940A-3   Sequence 3, Appli
        4   125.4   4.0   3692   4   US-09-077-940A-1   Sequence 1, Appli
        5   102   3.2   2278   4   US-09-976-594-1002   Sequence 1002, Ap
        6   98.6   3.1   121   4   US-09-833-381-202   Sequence 202, App
        7   98.6   3.1   2790   4   US-09-254-594-5   Sequence 5, Appli
        8   98.6   3.1   3432   4   US-09-254-594-4   Sequence 4, Appli
        9   89.8   2.9   2787   4   US-09-254-594-2   Sequence 2, Appli
       10   89.8   2.9   3195   4   US-09-254-594-1   Sequence 1, Appli
       11   84.2   2.7   4286   4   US-09-976-594-632   Sequence 632, App

12	78.6	2.5	3560	1	US-08-121-713D-59	Sequence 59, Appl
13	78.6	2.5	3560	1	US-08-835-268-59	Sequence 59, Appl
14	78.6	2.5	3560	2	US-09-060-692-59	Sequence 59, Appl
15	78.6	2.5	3560	3	US-08-833-391-59	Sequence 59, Appl
16	78.6	2.5	3560	4	US-09-060-610-59	Sequence 59, Appl
17	78.6	2.5	3560	5	PCT-US94-10151A-59	Sequence 59, Appl
18	78.2	2.5	1923	4	US-09-653-274-12	Sequence 12, Appl
19	78.2	2.5	3261	4	US-09-653-274-5	Sequence 5, Appli
20	78.2	2.5	3694	4	US-09-653-274-3	Sequence 3, Appli
21	69.8	2.2	2670	1	US-08-121-713D-61	Sequence 61, Appl
22	69.8	2.2	2670	1	US-08-835-268-61	Sequence 61, Appl
23	69.8	2.2	2670	2	US-09-060-692-61	Sequence 61, Appl
24	69.8	2.2	2670	3	US-08-833-391-61	Sequence 61, Appl
25	69.8	2.2	2670	4	US-09-060-610-61	Sequence 61, Appl
26	69.8	2.2	2670	5	PCT-US94-10151A-61	Sequence 61, Appl
27	63.8	2.0	2601	1	US-08-121-713D-53	Sequence 53, Appl
28	63.8	2.0	2601	1	US-08-835-268-53	Sequence 53, Appl
29	63.8	2.0	2601	2	US-09-060-692-53	Sequence 53, Appl
30	63.8	2.0	2601	3	US-08-833-391-53	Sequence 53, Appl
31	63.8	2.0	2601	4	US-09-060-610-53	Sequence 53, Appl
32	63.8	2.0	2601	5	PCT-US94-10151A-53	Sequence 53, Appl
33	62.6	2.0	7218	1	US-08-232-463-14	Sequence 14, Appl
34	62	2.0	2854	1	US-08-121-713D-57	Sequence 57, Appl
35	62	2.0	2854	1	US-08-835-268-57	Sequence 57, Appl
36	62	2.0	2854	2	US-09-060-692-57	Sequence 57, Appl
37	62	2.0	2854	3	US-08-833-391-57	Sequence 57, Appl
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41	50.2	1.6	2504	1	US-08-121-713D-63	Sequence 63, Appl
42	50.2	1.6	2504	1	US-08-835-268-63	Sequence 63, Appl
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44	50.2	1.6	2504	3	US-08-833-391-63	Sequence 63, Appl
45	50.2	1.6	2504	4	US-09-060-610-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-09-300-958A-24
; Sequence 24, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624

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   Query Match              7.3%;   Score 230;   DB 4;   Length 2433;
   Best Local Similarity   50.2%;   Pred. No. 4.5e-51;
   Matches  906;  Conservative    0;  Mismatches  805;  Indels   93;  Gaps   10;

Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
              | ||  ||  |||||       ||||||||| || || || ||||||||| ||||| ||| |  | |
Db         53 CCCTTCTGCTGAGCCAGGATGGAAAGACGCTGTATGTGGGGGCCCGAGAGGCCCTCTTTG 112

Qy        361 CCTTGGATATCCAGGATCCAGGGGTCCC---CAGGCTAAAGAACATGATACCGTGGCCAG 417
              |  |  | | | | |        | ||  | ||    | |  | ||| ||||      |
Db        113 CACTTAACAGCAACCTCAGCTTCTTGCCAGGCGGGGAGTACCAAGAGCTACTGTGGAGTG 172

Qy        418 CCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTT 477
              |   ||      |   |||     | ||    ||| |||    |||  |     ||  | |||
Db        173 CAGATGCTGACAGGAAGCAGCAGTGCAGCTTCAAGGGCAAGGACCCAAAGCGTGACTGTC 232

Qy        478 TCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCT 537
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Db        233 AAAACTACATCAAGATCCTCCTGCCACTCAACAGCAGCCACCTGCTCACCTGTGGCACGG 292

Qy        538 TCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCT 597
              ||||||||||||     ||| | | |||||  |        |      |        |     |
Db        293 CCGCCTTCAGCCCCCTGTGTGCTTACATTCACATAGCGAGCTTTACTTTAGCCCAAGATG 352

Qy        598 CGGAGGACAAGGTCAT------GGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
              ||   |  || |||||        ||| || || || ||  |  ||||||||||||||||      ||
Db        353 AGGCCGGTAATGTCATTCTGGAGGATGGCAAGGGTCATTGTCCCTTTGACCCCAACTTCA 412

Qy        652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
              ||    ||||||  |  ||||  |||||    ||| ||  |||| ||  |  |  | ||||| ||
Db        413 AGTCCACGGCTCTGGTGGTTGATGGTGAGCTGTACACTGGAACAGTCAGTAGCTTCCAGG 472

Qy        712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
              | |  || ||  |   || ||| |  | | | |    | |  | |||||| || | ||
Db        473 GAAACGACCCAGCCATTTCCCGGAGCCAGAGTTCCCGCCC---CACCAAGACTGAGAGCT 529

Qy        772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
              ||||    |||||| ||  |         ||||  | |  | ||| |  |              | |
Db        530 CCCTCAACTGGCTACAAGACCCTGCCTTTGTGGCCTCGGCTACGTCCCCCGAGAGCCTGG 589

Qy        832 ------------------------TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGT 864
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Qy        865 TTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGG 924
              ||||  |||||||||||     |  |    || || || |  ||||||| |||   || | ||
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Qy    925  GCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCA  984
           | ||  ||    |  ||  ||||| |    ||||||  |||| ||  ||||| |||||  ||  |||
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Qy   1042  ATTCTCCCACAGCTCCCCACATCTA------CGCAGTCTTCACCTCCCAGTGGCAGGTTG  1095
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           | ||    |||||  | | |||| | ||||  || ||   | |||  ||| || ||  ||  |
Db    950  ACGGCCTGTACAAGAAAGTAAACAGAGAGACACAGCAGTGGTATACCGAGACCCACCAGG  1009

Qy   1216  AGACCAACCCCCGGCCAGGCAGTTG------------------------------CT  1242
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           |     |     | | ||    | |||| |||| | |||||| ||  ||| |||||||||
Db   1070  CGTCCCTGCAGCTCCCAGACCGAGTGCTGAACTTCCTCAAGGATCACTTCTTGATGGATG  1129

Qy   1303  AGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG  1362
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Db   1130  GGCAGGTCCGCAGTCGCCTGCTGCTGCTGCAGCCCAGAGCCCGCTACCAGCGTGTGGCTG  1189

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Qy   1423  CAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGA  1482
           || ||  || |||||| || |||    | |  |   | || | |   | || | | || |||
Db   1247  ATGGCCGCCTGCACAAAGCAGTG---ACCCTGAGCTCCAGAGTCCACATCATTGAGGAGC  1303

Qy   1483  TTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTG  1542
           | ||| | |||||| |     | ||||| | ||||||| |  | | | |     |||
Db   1304  TGCAGATCTTCCCTCAAGGACAGCCTGTGCAGAACCTGCTCTTGGACAGCCATGGGGGAC  1363

Qy   1543  CAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCT  1602
           ||| || | |    || |   ||  || | |      |||||| |||||||||| ||  | |
Db   1364  TGTTGTATGCCTCCTCCCATTCCGGGGTGGTGCAAGTGCCCGTAGCCAACTGCAGCCTGT  1423

Qy   1603  ATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGT  1662
           |     | ||||| |||||  |||| | || || || || ||||||| |||| ||||||
Db   1424  ACCCAACCTGTGGAGACTGCCTCCTGGCTCGAGACCCCTACTGCGCCTGGACTGGCTCTG  1483

Qy   1663  CCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGC  1722
           || | |      |||  | | || |  ||| ||| |||| ||  | |  | |||
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Db    1544 TTGAGGGTGCCAGTGTCAAGGAACTCTGCAAGAATTCCTCATACAAGGCCCGGTTTCTTG 1603

Qy    1783 GCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCT 1842
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Db    1604 TGCCAGGTAAGCCATGTAAACAAGTCCAGATCCAACCAAACACAGTGAACACCCTGGCCT 1663

Qy    1843 GCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAG 1902
             |||| | ||| |||  | ||||| ||        ||| ||       ||| ||||| |
Db    1664 GCCCACTCCTCTCAAACCTGGCCACTCGGCTCTGGGTGCACAATGGAGCCCCAGTCAATG 1723

Qy    1903 AAGCCTCTTCCACTGTCTA------CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAG 1956
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Db    1724 CCTCTGCCTCCTGCCGCGTGTTACCCACCGGGGACCTGCTGCTGGTGGGCAGCCAGCAGG 1783

Qy    1957 TTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCT 2016
             |   |||  | | |||||| ||| | |   || | || ||       | | ||||  |  ||
Db    1784 GTTTGGGGGTGTTCCAGTGTTGGTCGATAGAAGAAGGATTCCAGCAGCTTGTGGCCAGCT 1843

Qy    2017 ACTG 2020
             ||||
Db    1844 ACTG 1847


RESULT 2
US-08-556-422A-1
; Sequence 1, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
;  APPLICANT: HALL, Kathryn T.
;  APPLICANT:  FREEMAN, Gordon J.
;  APPLICANT:  SCHULTZE, Joachim L.
;  APPLICANT:  BOUSSIOTIS, Vassiliki
;  APPLICANT:  NADLER, Lee M.
;  TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
;  FILE REFERENCE: DFN-005CPA2
;  CURRENT APPLICATION NUMBER: US/08/556,422A
;  CURRENT FILING DATE:  1995-11-09
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 4157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (88)...(2673)
US-08-556-422A-1

   Query Match              4.9%;   Score 153.4;  DB 4;   Length 4157;
   Best Local Similarity   50.0%;   Pred. No. 1.4e-30;
    Matches  743;  Conservative    0;  Mismatches  636;  Indels  108;  Gaps   10;

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Qy   330  CTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCC  389
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Db   271  TTGTACATAGGTGCCCGGGAGGC------GGTCTTCGCTGTGAACGCACTCAACATCTCC  324

Qy   390  AGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTT  449
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Qy   450  AAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAAT  509
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Db   385  AAGGGGAAATCAAAACAGACAGAGTGCCTCAACTACATCCGGGTGCTGCAGCCACTCAGC  444

Qy   510  GTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAA  569
          | |||     || |||  || || ||| ||  ||| |||   || ||  ||| |  | |  |
Db   445  GCCACTTCCCTTTACGTGTGTGGGACCAACGCATTCCAGCCGGCCTGTGACCACCTGAAC  504

Qy   570  CTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAA  629
          |   | |   | |   |  || |       || ||           || |||||  |
Db   505  TTAACATCCTTTAAGTTTCTGGGGAAAAATGAAGAT-----------GGCAAAGGAAGA  552

Qy   630  AGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCT  689
          | |||||||||||| || ||||  | || |   | ||| |||  |||| |||||   || |||||
Db   553  TGTCCCTTTGACCCAGCACACAGCTACACATCCGTCATGGTTGATGGAGAACTTTATTCG  612

Qy   690  GGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAG  749
          || ||   | | || ||  |||| ||||| |||||| ||||| |       || |            |
Db   613  GGGACGTCGTATAATTTTTTGGGAAGTGAACCCATCATCTCCCGAAATTCTTCCCACAGT  672

Qy   750  CCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCA  809
          ||| |     |       |     ||| |     | | |  | || |     |||| |
Db   673  CCTCTGAGGACAGAATATGCAATCCCTTGGCTGAACGAGCCTAGTTTCGTGTTTGCTGAC  732

Qy   810  GCCATCCCTTCGACCCAGGTC--------------------------GTCTACTTCTTCTTC  845
          |  ||||      |  | ||  |                       ||||||||||||||||
Db   733  GTGATCCGAAAAAGCCCAGACAGCCCCGACGGCGAGGATGACAGGGTCTACTTCTTCTTC  792

Qy   846  GAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGA  905
          ||||     |     |||| ||| ||   |     ||| | | | | ||| | || |||
Db   793  ACGGAGGTGTCTGTGGAGTATGAGTTTGTGTTCAGGGTGCTGATCCCACGGATAGCAAGA  852

Qy   906  GTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTG  965
          || |||||| |||  |||||||| | |  ||||||||||| ||||| |||||| ||||||||
Db   853  GTGTGCAAGGGGGACCAGGGCGGCCTGAGGACCTTGCAGAAGAAATGGACCTCCTTCCTG  912

Qy   966  AAGGCCCAGCTGCTCTGCACCCAGCCGG---GGCAGCTGCCCTTCAACGTCATCCGCCAC  1022
          || |||| ||  ||||| ||| ||| |  |       || ||||||| ||  | ||| |
Db   913  AAAGCCCGACTCATCTGCTCCCGGCCAGACAGCGGCTTGGTCTTCAATGTGCTGCGGGAT  972

Qy   1023 GCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCC  1082
          |  ||  ||||||     ||       |  |  |  ||     |||| ||| ||||||||| |
Db   973  GTCTTCGTGCTCAGGTCCCCGGGCCTGAAGGTGCCTGTGTTCTATGCACTCTTCACCCCA  1032

Qy   1083 CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATT  1142
          ||| |  |    |  |||    |        | |    |  |||| |  |    | ||
Db   1033 CAGCTGAACAACGTGGGGCTGTCGGCAGTGTGCGCCTACAACCTGTC---CACAGCCGAG  1089

Qy   1143 GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG---------AAACTTCACGC  1193
```

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              ||      |||    |  ||||| ||||    ||   | ||  ||                      |
Db    1090 GAGGTCTTCTCCCACGGGAAGTACATGCAGAGCACCACAGTGGAGCAGTCCCACACCAAG 1149

Qy    1194 TGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGC--- 1250
              |||         ||||   ||||| |   |||| || ||||| ||    ||| |   ||
Db    1150 TGGGTGCGCTATAATGGCCCGGTACCCAAGCCGCGGCCTGGAGCGTGCATCGACAGCGAG 1209

Qy    1251 -------------------------------CCCTCCTCTGATAAGGCCCTGACCTTCATG 1280
                                           |   | || ||| | |||    ||| |
Db    1210 GCACGGGCCGCCAACTACACCAGCTCCTTGAATTTGCCAGACAAGACGCTGCAGTTCGTT 1269

Qy    1281 AAGGACCATTTCCTGATGGATGA---------GCAAGTGGTGGGGACGCCCCTGCTGGTG 1331
              ||  |||||        ||||||||||||          | | | |     | |||||   | | |
Db    1270 AAAGACCACCCTTTGATGGATGACTCGGTAACCCCAATAGACAACAGGCCCAGGTTAATC 1329

Qy    1332 AAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCAC 1391
              ||     |   ||| | || || | |  |  |||||      |||||| ||| ||||||
Db    1330 AAGAAAGATGTGAACTACACCCAGATCGTGGTGGACCGGACCCAGGCCCTGGATGGGAGT 1389

Qy    1392 AGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGT 1451
               | ||   ||||||||    |   | ||    ||  |  || ||||| ||   |     ||
Db    1390 GTCTATGATGTCATGTTTGTCAGCACAGACCGGGGGAGCTCTGCACAAAGCCATC---AGC 1446

Qy    1452 GGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTT 1511
               ||    |   || |||    |   | || ||||    ||||| ||||   |||   ||| || ||
Db    1447 CTCGAGCACGCTGTTCACATCATCGAGGAGACCCAGCTCTTCCAGGACTTTGAGCCAGTC 1506

Qy    1512 CGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGT------AGGCTTCTCAGGA 1565
              |  | |||||| ||||  |   | |    ||||          ||||||          ||||
Db    1507 CAGACCCTGCTGCTGTCTTCAAAGAAGGGCAACAGGTTTGTCTATGCTGGCTCTAACTCG 1566

Qy    1566 GGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTC 1625
              || ||         || || |   |||   ||||| |        | |   | ||| | |||||||||
Db    1567 GGCGTGGTCCAGGCCCCGCTGGCCTTCTGTGGGAAGCACGGCACCTGCGAGGACTGTGTG 1626

Qy    1626 CTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTG 1672
              || || |||||||||| ||||| ||||||   |||       |||||
Db    1627 CTGGCGCGGGACCCCTACTGCGCCTGGAGCCCGCCCACAGCGACCTG 1673
```

RESULT 3
US-09-077-940A-3
; Sequence 3, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 3524
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:

```
;    NAME/KEY: 5'UTR
;    LOCATION: (1)..(38)
;    OTHER INFORMATION:
;    NAME/KEY: 3'UTR
;    LOCATION: (2706)..(3524)
;    OTHER INFORMATION:
;    NAME/KEY: CDS
;    LOCATION: (39)..(2702)
;    OTHER INFORMATION:
US-09-077-940A-3

   Query Match              4.0%;   Score 126;   DB 4;   Length 3524;
   Best Local Similarity   55.3%;   Pred. No. 2.5e-23;
   Matches  315;  Conservative    0;  Mismatches  240;  Indels   15;  Gaps    3;

Qy        450 AAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAAT 509
              | |||| |    | ||| |||||  |||||| |  || ||| |   |      |
Db        390 ATGAAGGGCAAACAGGAGGGCGAGTGTCGAAACTTCGTAAAGGTGCTGCTCCTTCGGGAC 449

Qy        510 GTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAA 569
              |   ||  ||||   |||||  || |||||||||| ||| | || || | |
Db        450 GAGTCCACGCTCTTTGTGTGCGGTTCCAACGCCTTCAACCCGGTGTGCGCCAACTACAGC 509

Qy        570 CTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAA 629
                | |     | |||| |||| ||  ||  |    ||| || | | ||
Db        510 ATAGA------CACCCTGCAGCCCGTCGGAGACAA------CATCAGCGGTATGGCCCGC 557

Qy        630 AGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCT 689
              |||| | |||||| |||   || || |||| || |||||||||| |
Db        558 TGCCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACA 617

Qy        690 GGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAG 749
              | |||| | | | |||||||| | || ||| | || | |||| || || | | | |
Db        618 GCTACTGTTACCGACTTCCTAGCCATTGATGCTGTCATCTACCGCAGCCTCGGGGACAGG 677

Qy        750 CCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCA 809
              || ||| |||| || | | | | || || | |||||
Db        678 CCCACCCTGCGCACCGTGAAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCAT 737

Qy        810 GCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGAC 869
              ||  |     | |   |  ||||||||||||||||| ||||| || | |||||| ||
Db        738 GCGGTGGAGTGGGGGCAGCCATGTCTACTTCTTCTTCCGGGAGATTGCGATGGAGTTTAAC 797

Qy        870 TTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGC 929
              | | |||| | |    || || |||||  |||| |||||||| ||||||||| |||
Db        798 TACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAACGACGTGGGAGGC 857

Qy        930 GAAAAGC---TGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACC 986
               |    | ||||| ||||| ||||||| ||||||||||||| | ||| |||| |
Db        858 TCCCCCCGCGTGCTGGAGAAGCAGTGGACGTCCTTCCTGAAGGCGCGGCTCAACTGCTCT 917

Qy        987 CAGCCGGGGCAGCTGCCCTTCAACGTCATC 1016
              || || |   | ||| || ||| |
Db        918 GTACCCGGAGACTCCCATTTCTACTTCAAC 947


RESULT 4
```

US-09-077-940A-1
; Sequence 1, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3692
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(18)
;   OTHER INFORMATION:
;   NAME/KEY: CDS
;   LOCATION: (19)..(2682)
;   OTHER INFORMATION:
;   NAME/KEY: 3'UTR
;   LOCATION: (2683)..(3653)
;   OTHER INFORMATION:
;   NAME/KEY: polyA_site
;   LOCATION: (3654)..(3692)
;   OTHER INFORMATION:
US-09-077-940A-1

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    Query Match            4.0%;  Score 125.4;  DB 4;   Length 3692;
    Best Local Similarity  58.5%;  Pred. No. 3.7e-23;
    Matches  238;  Conservative    0;  Mismatches  166;  Indels    3;  Gaps     1;

Qy       611 CATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGT 670
                 |||     || |  | ||   ||||||| ||||||  ||     || || ||  ||||
Db       522 CATCAGTGGTATGGCCCGCTGCCCCTACGACCCCAAGCATGCCAATGTCGCCCTCTTCTC 581

Qy       671 GGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGAT 730
                 |||||||||||||  | |   || | |    |||||||  | ||  ||  | |   |
Db       582 AGATGGGATGCTCTTCACAGCCACAGTAACTGACTTCCTAGCCATCGACGCTGTTATCTA 641

Qy       731 GCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCA 790
                 || |  || ||   || |||   ||     || ||   |   |  |   |  |  ||
Db       642 CCGTAGCCTTGGGGACCGGCCCACACTGCGCACAGTAAAGCATGACTCCAAGTGGTTTAA 701

Qy       791 TGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGA 850
                 ||   | | ||||||||   ||  |    | |        ||||||||||||||||  |||
Db       702 AGAGCCATACTTTGTGCATGCGGTGGAGTGGGGAAGCCACGTCTACTTCTTCTTCCGGGA 761

Qy       851 GACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTG 910
                 ||  ||||  ||||||  |||  | | |  | | |   || || ||||| | || ||
Db       762 GATCGCCATGGAGTTTAACTATCTGGAAAAGGTGGTGGTGTCCCGTGTGGCCCGTGTATG 821

Qy       911 CAAGAATGACGTGGGCGG---CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAA 967
                 ||||||||| |||||||||   |  |  | ||||| ||||| ||||||| |||||||||||
Db       822 CAAGAATGATGTGGGCGGCTCCCCACGGGTGCTGGAGAAGCAGTGGACTTCCTTCCTGAA 881
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Qy       968 GGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA 1014
             |||| |||   |||| ||  ||| ||| |   | |||| || |||
Db       882 GGCCCGGCTCAACTGCTCCGTGCCTGGGGACTCACACTTCTACTTCA 928


RESULT 5
US-09-976-594-1002
; Sequence 1002, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH
STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 1002
;   LENGTH: 2278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 411373.7
US-09-976-594-1002

  Query Match              3.2%;  Score 102;  DB 4;  Length 2278;
  Best Local Similarity   50.0%;  Pred. No. 4.9e-17;
  Matches  339;  Conservative   0;  Mismatches  330;  Indels   9;  Gaps    3;

Qy       618 GGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGG 677
             ||||  |  |  | |||| | ||| ||  ||    |    || | || |  |||||
Db       761 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 820

Qy       678 ATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACA 737
             |  || || || |  ||   ||| ||||||| | || |||  | || |   || |
Db       821 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 880

Qy       738 CTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCC 797
             || |||       ||| |||   |||||  |||    |    | || | |  |
Db       881 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 940

Qy       798 TCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCC 857
             | |||||||    |||| |    ||      |     |||||||||||||| ||| | |||
Db       941 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 1000

Qy       858 AGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAT 917
             |||| | ||  | | | |||        |  | |||||||  || || |||||||
Db      1001 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1060

Qy       918 GACGTGGGCGG---CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAG 974
             ||  |||| ||    |||   | ||| |||| ||||||| | |||||||||||||||| |
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Db     1061  GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1120

Qy      975  CTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTC 1034
              ||  ||||| |     || || |    |   || | ||| |  | | || |    |
Db     1121  TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1180

Qy     1035  CCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTT 1094
               |    |  |  ||  | |    | |     |  |  |    || |        |     |
Db     1181  GATGTGATTCGTATCAACGGGCGTGATGT---TGTCCTGGCAACGTTTTCTACACCTTAT 1237

Qy     1095  GGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTT 1154
              | | |  |     | ||||| || |||||||     |  | |||||||   |||| |||
Db     1238  AACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTT 1297

Qy     1155  AAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTAC---TTATAGGGGC 1211
              |  |||| || ||| ||  |||         ||| | |||||| |    |   |    |
Db     1298  ACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAA 1357

Qy     1212  CCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTG 1271
              | |   | || ||| ||||||| | ||  | |       ||||||  || |
Db     1358  CGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCA 1417

Qy     1272  ACCTTCATGAAGGACCAT 1289
              |||| ||   ||  || |
Db     1418  ACCTCCAATGAGTTCCCT 1435


RESULT 6
US-09-833-381-202
; Sequence 202, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
;   LENGTH: 121
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-833-381-202

  Query Match               3.1%;   Score 98.6;   DB 4;   Length 121;
  Best Local Similarity   88.4%;   Pred. No. 9e-17;
  Matches  107;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      794  CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 853
              |||||||||||||||| ||| ||||||||| |||||| | || ||||||||||||| |||||||
Db        1  CGCCTCCTTTGTGGAAGACATCCCTTCTACCCACGGCGCCTACTTCTTCTTCCAGGAGAC 60

Qy      854  AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA 913
              |||||||||||| ||||   |||||||||||||||||||||  || |||||||||||||||
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Db          61 AGCCAGCGAGTTAGACTCTTTTGAGAGGCTCCACACATAATGGTTGGCTAGAGTCTGCAA 120

Qy         914 G 914
               |
Db         121 G 121
```

RESULT 7
US-09-254-594-5
; Sequence 5, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 2790
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Child Brain
;   NAME/KEY: CDS
;   LOCATION: (1)..(2790)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-5

  Query Match   3.1%;   Score 98.6;   DB 4;   Length 2790;
  Best Local Similarity 50.1%;   Pred. No. 4.3e-16;
  Matches 369; Conservative   0; Mismatches 344; Indels 24; Gaps   4;

Qy   472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
               |||| | ||||| || ||||| || ||| | | | | ||| | |||| |
Db   359 AGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCTGTG 418

Qy   532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
               | || | | |||||||||||| || | | | || | | ||
Db   419 GAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGAT-----------AACTTCGC 466

Qy   592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
                   ||||| ||| || || || | | | | |||||||||| || | ||
Db   467 TGCAGCAGGAGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGT 526

Qy   652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
                 | ||| |||| | || || || | || || || | || | |||| ||
Db   527 CCAACGTGGCCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGG 586

Qy   712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
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                    ||||||  |   |    |      | |  || ||  |||||||    |||    ||| ||| |
Db        587 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 646

Qy        772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
                |  |  |  | || | || |   |||||| |||| |          |     |
Db        647 ATGACTCCAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATG 706

Qy        832 TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 891
                |||||||||||||||   |||   |    |||  ||     | | || | | ||   |
Db        707 TCTACTTCTTCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCT 766

Qy        892 CGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGAAGA 948
                | || || ||  |||| || ||    |||| |||||||||     | |     || |
Db        767 CCCGCGTAGCCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCC 826

Qy        949 AGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCA 1008
                | |||||  |||||||||||| | ||| |||| |   || ||| |    | |||
Db        827 ACTGGACATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCT 886

Qy       1009 A---CGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
                |    |    |    || || |       || | |    |          |      |||
Db        887 ATTTGATGTTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCT 946

Qy       1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
                |  |||||||||| |||||       |         | | |  ||||||| || || ||||
Db        947 TTGGGGTCTTCACCACCCAGACCAA------TAGCATCCCTGGCTCTGCCGTCTGCGCCT 1000

Qy       1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
                ||| ||  || ||||| |||| ||| |||| ||| |||| || | ||| |||| || |
Db       1001 TCTACCTGGATGAGATTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1060

Qy       1186 CTTCACGCTGGACTACT 1202
                |       |||||||| ||
Db       1061 ATGGGGCCTGGACTCCT 1077


RESULT 8
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
;   APPLICANT:  KIMURA, Toru
;   APPLICANT:  KIKUCHI, Kaoru
;   TITLE OF INVENTION:   NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
;   FILE REFERENCE:   0020-4527P
;   CURRENT APPLICATION NUMBER: US/09/254,594
;   CURRENT FILING DATE:  1999-05-11
;   NUMBER OF SEQ ID NOS:   13
;   SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 3432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Child Brain
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;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(187)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: (188)..(2977)
;   OTHER INFORMATION: CDS; Identification Method: E
;   NAME/KEY: 3'UTR
;   LOCATION: (2978)..(3407)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: polyA_signal
;   LOCATION: (3408)..(3432)
;   OTHER INFORMATION: Identification Method: E
US-09-254-594-4

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     Query Match              3.1%;   Score 98.6;  DB 4;   Length 3432;
     Best Local Similarity   50.1%;   Pred. No. 4.8e-16;
     Matches  369;  Conservative    0;  Mismatches  344;  Indels   24;  Gaps    4;

Qy         472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
               |||| | ||||| || ||||| || ||| | |    |     |    ||| |||| |
Db         546 AGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCTGTG 605

Qy         532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
               | || | | |||||||||| || | | || |          | ||
Db         606 GAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGAT-----------AACTTCGC 653

Qy         592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
               |||||    |||    ||    ||   | | | | ||||||||| || | ||
Db         654 TGCAGCAGGAGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGT 713

Qy         652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
               |    |||  |||| | || || | || || || | | ||   | |||| ||
Db         714 CCAACGTGGCCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGG 773

Qy         712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
               ||||||  |  |  |      | |  || || |||||||    |||    ||| ||||  |
Db         774 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 833

Qy         772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
                |   | |   || | |  || |   ||||||    |||  |        | |    |
Db         834 ATGACTCCAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATG 893

Qy         832 TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 891
               |||||||||||||||| |||   |     | ||| ||   | | || | | | ||    |
Db         894 TCTACTTCTTCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCT 953

Qy         892 CGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGAAGA 948
               | || || || |||| || || ||    |||| ||||||||| | |    || |
Db         954 CCCGCGTAGCCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCC 1013

Qy         949 AGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCA 1008
               | ||||| |||||||||||||||| | ||  |||| | ||| | || ||| | | |||
Db        1014 ACTGGACATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCT 1073

Qy        1009 A---CGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
               |    |   |   || || | ||  | | |   | || ||   |         | |||
Db        1074 ATTTTGATGTTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCT 1133
```

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Qy      1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
                 |  ||||||||| |||||      |         | | |   |||||| || || ||||
Db      1134 TTGGGGTCTTCACCACCCAGACCAA------TAGCATCCCTGGCTCTGCCGTCTGCGCCT 1187

Qy      1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
                 |||  ||    || |||||  ||||  ||| ||||  || | ||| |||  ||   |
Db      1188 TCTACCTGGATGAGATTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1247

Qy      1186 CTTCACGCTGGACTACT 1202
                 |      ||||||| ||
Db      1248 ATGGGGCCTGGACTCCT 1264


RESULT 9
US-09-254-594-2
; Sequence 2, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
;  APPLICANT:  KIMURA, Toru
;  APPLICANT:  KIKUCHI, Kaoru
;  TITLE OF INVENTION:   NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
;  FILE REFERENCE:   0020-4527P
;  CURRENT APPLICATION NUMBER: US/09/254,594
;  CURRENT FILING DATE:  1999-05-11
;  NUMBER OF SEQ ID NOS:   13
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Brain
;   NAME/KEY: CDS
;   LOCATION: (1)..(2787)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-2

   Query Match              2.9%;   Score 89.8;  DB 4;  Length 2787;
   Best Local Similarity   50.1%;   Pred. No. 9.5e-14;
   Matches  369;  Conservative   0;  Mismatches  347;  Indels   21;  Gaps    5;

Qy       472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
                 | || | ||||| |||||||||| || ||| | |    |       |||    |||| |
Db       356 AATGCTACAACTACATCCGTGTTCTTGTTCCCTGGGACTCGCAGACACTCCTTGCCTGTG 415

Qy       532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
                 |  ||        ||||||||||||| |||  |  |  ||   |   |    |  | |
Db       416 GAACAAATTCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAAC------ 469

Qy       592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
                 |||||    |||    ||    ||   |||  | | |||||||||||  || | ||
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Db     470 ------AGGAGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCTTTGATGCCACCCAGT 523

Qy     652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
               |  |||  |||  |  || || |   |  || || |  ||      | |||| ||
Db     524 CCACTGTGGCCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCCAGG 583

Qy     712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
               ||||||  |  |   |     || |  || ||| | |||||    |||    |  || |
Db     584 CCAGTGATGCTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCCACTCCGTTCTGCAAAGT 643

Qy     772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCAT---CCCTTCGACCCAGG 828
               | |  |  || ||  || |  |||||| || |  |  ||| ||| |
Db     644 ATGACTCCAAGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATG 703

Qy     829 TCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACA 888
               ||  ||  |||  |    ||| || |       |   |   |  | | | |||| | ||
Db     704 TCTACTTCTTTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCGGCCTGGGGAGGGTGCAGT 763

Qy     889 CATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGA 945
               ||  ||||||||  | || || || ||   |||| |||| ||| |  | |     || |
Db     764 TTTCCCGGGTGGCCCGGGTGTGTAAACGTGACATGGGTGGCTCACCACGGGCCTTGGATC 823

Qy     946 AGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCT 1005
               |  ||||| |||||||| |||       ||| |  |||| ||  || ||| |    |||
Db     824 GCCACTGGACATCCTTCCTTAAGCTGAGGCTCAACTGCTCCGTCCCTGGGGACTCTACCT 883

Qy    1006 TCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
               || || |       |  |  | |||||| |   ||| |  || ||  | ||| | | |
Db     884 TCTAC-TTTGATGTCTTACAGTCCTTAACTGGGCCTGTGAACCTGCATGGGCGCTCTGC- 941

Qy    1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
               |    |    ||| |   |||     ||   |    ||   | | ||||| || || ||||
Db     942 -CCTCTTTGGGGTCTTCACTACTCAGACCAATAGCATTCCTGGGTCTGCAGTCTGCGCCT 1000

Qy    1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
               |||   ||   |||||||||||||||| |||| |||| || |  | ||| |||  ||  |
Db    1001 TCTACCTAGATGACATTGAACGTGGCTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1060

Qy    1186 CTTCACGCTGGACTACT 1202
               |      |||||||| ||
Db    1061 ATGGGGCCTGGACTCCT 1077
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RESULT 10
US-09-254-594-1
; Sequence 1, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

Query Match   2.9%;   Score 89.8; DB 4; Length 3195;
Best Local Similarity   50.1%;   Pred. No. 1e-13;
Matches 369; Conservative   0; Mismatches 347; Indels   21; Gaps   5;

```
Qy       472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
             | || | ||||| ||||||||| || ||| | |    |      |||    |||| |
Db       406 AATGCTACAACTACATCCGTGTTCTTGTTCCCTGGGACTCGCAGACACTCCTTGCCTGTG 465

Qy       532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
             | ||        ||||||||||||| |||  | |  ||   |   | |  |    | |
Db       466 GAACAAATTCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAAC------ 519

Qy       592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
               ||||| |||    ||    ||    |||   | | ||||||||| || | ||
Db       520 ------AGGAGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCTTTGATGCCACCCAGT 573

Qy       652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
               |   |||   |||  |  | || | |  | || || |  ||         | |||| ||
Db       574 CCACTGTGGCCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCCAGG 633

Qy       712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
             ||||||  |   |    |   |  || ||| | |||||     |||     | |  || |
Db       634 CCAGTGATGCTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCCACTCCGTTCTGCAAAGT 693

Qy       772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCAT---CCCTTCGACCCAGG 828
             | | | || || || || || | | ||||| || | |  |    | |    ||| |
Db       694 ATGACTCCAAGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATG 753

Qy       829 TCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACA 888
             || || ||| |    ||| || |  |    | | | || || ||||| | ||
Db       754 TCTACTTCTTTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCGGCCTGGGGAGGGTGCAGT 813

Qy       889 CATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGA 945
             || |||||||| | || || || ||    |||| |||| ||| |  | |    || |
Db       814 TTTCCCGGGTGGCCCGGGTGTGTAAACGTGACATGGGTGGCTCACCACGGGCCTTGGATC 873

Qy       946 AGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCT 1005
             | ||||| ||||||| |||    |||  |||| || || | || | || ||     |||
Db       874 GCCACTGGACATCCTTCCTTAAGCTGAGGCTCAACTGCTCCGTCCCTGGGGACTCTACCT 933
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```
Qy      1006 TCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
             || || |       | |     | ||||| |   ||| |  || ||    | | |   |
Db       934 TCTAC-TTTGATGTCTTACAGTCCTTAACTGGGCCTGTGAACCTGCATGGGCGCTCTGC- 991

Qy      1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
             |     |     || |     |||      | |     | ||||| || || ||||
Db       992 -CCTCTTTGGGGTCTTCACTACTCAGACCAATAGCATTCCTGGGTCTGCAGTCTGCGCCT 1050

Qy      1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
             |||  ||     ||||||||||||| |||| |||| |||| || | ||| |||  ||  |
Db      1051 TCTACCTAGATGACATTGAACGTGGCTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1110

Qy      1186 CTTCACGCTGGACTACT 1202
              |      ||||||| ||
Db      1111 ATGGGGCCTGGACTCCT 1127


RESULT 11
US-09-976-594-632
; Sequence 632, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH
STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 632
;   LENGTH: 4286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 238322.6
US-09-976-594-632

  Query Match             2.7%;  Score 84.2;  DB 4;  Length 4286;
  Best Local Similarity   50.3%;  Pred. No. 3.6e-12;
  Matches  273;  Conservative    0;  Mismatches  253;  Indels   17;  Gaps    2;

Qy       472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
             |||| | ||||| || ||||| || ||| | |   |   |       |||     |||| |
Db       611 AGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCTGTG 670

Qy       532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
             | ||   | | ||||||||||| ||  |   | ||  |                  | ||
Db       671 GAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGAT-----------AACTTCGC 718

Qy       592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
             |||||   ||| |  || || | |.|  | | ||||||||||| || | ||
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```
Db       719 TGCAGCAGGAGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGT 778

Qy       652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
                 |   |||   |||| |  || || |  || || || |  ||         |  |||| ||
Db       779 CCAACGTGGCCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGG 838

Qy       712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
                 ||||||  |  |   |       | |  || ||  |||||||    |||     ||| ||| |
Db       839 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 898

Qy       772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
                 |  |  |  ||  |  ||  |   ||||||   |||  |          |           |
Db       899 ATGACTCCAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATG 958

Qy       832 TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 891
                 |||||||||||||||   |||     |      ||| ||    | | |||| | ||      |
Db       959 TCTACTTCTTCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAGGGTGCAGTTCT 1018

Qy       892 CGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGA--- 948
                 | || || ||   |||| || ||    |||| |||||||||     |    |       |
Db      1019 CCCGCGTAGCCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTTCGGGTCTTGGTACCG 1078

Qy       949 --AGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTT 1006
                 | |||||| |||||||||||    | |||    |||| |      || ||| |     | ||
Db      1079 CCACTGGACATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTT 1138

Qy      1007 CAA 1009
                 | |
Db      1139 CTA 1141


RESULT 12
US-08-121-713D-59
; Sequence 59, Application US/08121713D
; Patent No. 5639856
;   GENERAL INFORMATION:
;     APPLICANT:  Goodman, Corey S.
;     APPLICANT:  Kolodkin, Alex L.
;     APPLICANT:  Matthes, David
;     APPLICANT:  Bentley, David R.
;     APPLICANT:  O'Connor, Timothy
;     TITLE OF INVENTION:  The Semaphorin Gene Family
;     NUMBER OF SEQUENCES:  100
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;       STREET:  268 Bush Street, Suite 3200
;       CITY:  San Francisco
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/121,713D
```

; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3560 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1953
US-08-121-713D-59

   Query Match   2.5%;   Score 78.6; DB 1; Length 3560;
   Best Local Similarity   49.2%;   Pred. No. 1e-10;
   Matches 358; Conservative   0; Mismatches 324; Indels   45; Gaps   4;

Qy   612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
              | | | ||| | | |||||| || || |||||| || |||| |||
Db   139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198

Qy   672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
              || || ||||| ||||| || | ||| ||||| || || || |
Db   199 GACAACGAACTGTATTCCGGTACCGTGGCGGATTTCAGTGGCAGCGATCCGATTATC--- 255

Qy   732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
                          | || | ||| |||||||| | | | || | |
Db   256 ------------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303

Qy   792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
              | | ||||||| | | | | | | | |||||| |||||||| |||
Db   304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363

Qy   852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
              || ||| |||||| | || || | | ||||| || || | ||||||
Db   364 ACCGCCGTTGAGTTTATCAACTGTGGCAAGGCGATTTATTCGCGCGTTGCCCGCGTCTGC 423

Qy   912 AAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCC 971
              || ||| || ||| | | | | | ||||| ||||||| ||| ||
Db   424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483

Qy   972 CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA----------------TC 1016
              | || |||| || || || | || ||| || | |
Db   484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543

Qy   1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
              || | ||| | | | || | | |||||||| |||||||
Db   544 AGCAATCTGGTGGAGGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603

```
Qy    1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
                | | | | | |   |         | |       |||| ||||||||||||||| | ||| |
Db     604 AACACGCCGAGCAA------CTCAATTCCCGGCTCAGCGGTTTGTGCCTTTGCCCTCCAG 657

Qy    1137 GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTG- 1195
                |||||||    |    ||| ||||  | | ||| |||  ||        | ||   |||
Db     658 GACATTGCCGATACGTTTGAGGGTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG 717

Qy    1196 --------GACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTG 1247
                   ||  |       | ||  || ||   |      ||| | | |       |       |
Db     718 CTGCCAGTGAACAACGCCAAGGTACCCGATCCTCGACCCGGTTCCTGTCACAACGATTCG 777

Qy    1248 GGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAA 1307
                | |    | |||      | |||| ||||||| ||      |||| || ||||| ||| |
Db     778 AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy    1308 GTGGTGG 1314
                ||| ||
Db     838 GTGCCGG 844


RESULT 13
US-08-835-268-59
; Sequence 59, Application US/08835268
; Patent No. 5807826
;  GENERAL INFORMATION:
;     APPLICANT:  Goodman, Corey S.
;     APPLICANT:  Kolodkin, Alex L.
;     APPLICANT:  Matthes, David
;     APPLICANT:  Bentley, David R.
;     APPLICANT:  O'Connor, Timothy
;     TITLE OF INVENTION:  The Semaphorin Gene Family
;     NUMBER OF SEQUENCES:  100
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;       STREET:  268 Bush Street, Suite 3200
;       CITY:  San Francisco
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/835,268
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/121,713
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Osman, Richard A.
;       REGISTRATION NUMBER:  36,627
;       REFERENCE/DOCKET NUMBER:  B94-002-1
```

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   Query Match              2.5%;   Score 78.6;  DB 1;  Length 3560;
   Best Local Similarity   49.2%;   Pred. No. 1e-10;
   Matches  358;  Conservative    0;  Mismatches  324;  Indels  45;  Gaps    4;

Qy       612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
             | | | ||| | |       ||||||  || ||   |||||||    || ||||  |||
Db       139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198

Qy       672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
             ||        || |||||| ||||| ||   | |||  |||||| || || || ||   |
Db       199 GACAACGAACTGTATTCCGGTACCGTGGCGGATTTCAGTGGCAGCGATCCGATTATC--- 255

Qy       732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
                         | || |   ||| |||||||| | |   ||      | |
Db       256 -----------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303

Qy       792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
             |   |   |||||||       |   |   |   |  | ||||| |||||||   |||
Db       304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363

Qy       852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
             || |||   ||||||   | || ||  | |           ||||| || ||  | ||||||
Db       364 ACCGCCGTTGAGTTTATCAACTGTGGCAAGGCGATTTATTCGCGCGTTGCCCGCGTCTGC 423

Qy       912 AAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCC 971
             ||    ||| || ||| || | | | |  |||||| ||||| | |||||||| ||| ||
Db       424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483

Qy       972 CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA---------------TC 1016
             |   ||  |||| ||  || ||  |  || ||| || | |                  |
Db       484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543

Qy      1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
             || |   |||   |    |   | ||    |    | ||||||| ||||||||
Db       544 AGCAATCTGGTGGAGGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603

Qy      1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
             | | | | |  |        |  |   |   |||| |||||||||||||||| | ||| |
Db       604 AACACGCCGAGCAA------CTCAATTCCCGGCTCAGCGGTTTGTGCCTTTGCCCTCCAG 657

Qy      1137 GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTG- 1195
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Db      658  GACATTGCCGATACGTTTGAGGGTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG 717

Qy     1196  --------GACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTG 1247
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Qy     1248  GGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAA 1307
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Db      778  AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy     1308  GTGGTGG 1314
                 | | |    | |
Db      838  GTGCCGG 844


RESULT 14
US-09-060-692-59
; Sequence 59, Application US/09060692
; Patent No. 5935865
;   GENERAL INFORMATION:
;     APPLICANT:  Goodman, Corey S.
;     APPLICANT:  Kolodkin, Alex L.
;     APPLICANT:  Matthes, David
;     APPLICANT:  Bentley, David R.
;     APPLICANT:  O'Connor, Timothy
;     TITLE OF INVENTION:  The Semaphorin Gene Family
;     NUMBER OF SEQUENCES:  100
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;       STREET:  268 Bush Street, Suite 3200
;       CITY:  San Francisco
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/060,692
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/121,713
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Osman, Richard A.
;       REGISTRATION NUMBER:  36,627
;       REFERENCE/DOCKET NUMBER:  B94-002-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415)343-4341
;       TELEFAX:  (415) 343-4342
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  59:
;     SEQUENCE CHARACTERISTICS:
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   Query Match              2.5%;   Score 78.6;  DB 2;  Length 3560;
   Best Local Similarity   49.2%;   Pred. No. 1e-10;
   Matches  358;  Conservative   0;  Mismatches  324;  Indels  45;  Gaps    4;


Qy        612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
              | | | ||| | |        |||||| || ||   |||||   ||  |||| |||
Db        139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198


Qy        672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
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Db        199 GACAACGAACTGTATTCCGGTACCGTGGCGGATTTCAGTGGCAGCGATCCGATTATC--- 255


Qy        732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
                         | || |     ||| ||||||| | |    ||          |   |  |
Db        256 -----------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303


Qy        792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
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Db        304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363


Qy        852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
              || |||     |||||| | || || ||          ||||| || || | ||||||
Db        364 ACCGCCGTTGAGTTTATCAACTGTGGCAAGGCGATTTATTCGCGCGTTGCCCGCGTCTGC 423


Qy        912 AAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCC 971
              ||     |||    ||  ||   | |    |  |  |||  ||||||| |||||| ||| ||
Db        424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483


Qy        972 CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA---------------TC 1016
              |  ||    |||| ||  || || |  || ||| || | |                    |
Db        484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543


Qy       1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
              || |   ||| |  | | |   | ||    |      | |   | ||||||| |||||||
Db        544 AGCAATCTGGTGGAGGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603


Qy       1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
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Db        604 AACACGCCGAGCAA------CTCAATTCCCGGCTCAGCGGTTTGTGCCTTTGCCCTCCAG 657


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Db     778 AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy    1308 GTGGTGG 1314
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Db     838 GTGCCGG 844
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; Sequence 59, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
;   APPLICANT: Goodman, Corey S.
;   APPLICANT: Kolodkin, Alex L.
;   APPLICANT: Matthes, David
;   APPLICANT: Bentley, David R.
;   APPLICANT: O'Connor, Timothy
;   TITLE OF INVENTION: The Semaphorin Gene Family
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 268 Bush Street, Suite 3200
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/833,391
;   FILING DATE:
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/121,713
;   FILING DATE: 13-SEP-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Osman, Richard A.
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: B94-002-1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)343-4341
;   TELEFAX: (415) 343-4342
;   TELEX:
; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3560 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:

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;      NAME/KEY: CDS
;      LOCATION: 1..1953
US-08-833-391-59

     Query Match              2.5%;   Score 78.6;  DB 3;  Length 3560;
     Best Local Similarity   49.2%;   Pred. No. 1e-10;
     Matches  358;  Conservative    0;  Mismatches  324;  Indels  45;  Gaps     4;

Qy        612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
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Qy        672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
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Qy        732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
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Db        256 -----------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303

Qy        792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
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Db        304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363

Qy        852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
              || |||   |||||| | || || | |          ||||| || || | |||||||
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Db        424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483

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Db        484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543

Qy       1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
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Qy       1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
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Qy       1196 --------GACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTG 1247
                      || |     | || || || |    |||  | |        |          |
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Qy       1248 GGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAA 1307
              | |    | |||    | ||||  | |||| |||||| || |||| || ||||| ||| |
Db        778 AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy       1308 GTGGTGG 1314
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Db      838 GTGCCGG 844
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Job time : 222 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004   Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:44:40 ; Search time 1271 Seconds
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Perfect score: 3143
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Searched: 2947324 seqs, 2269024515 residues

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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

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No.    Score  Match  Length  DB   ID                        Description
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  2    3143   100.0   3143   12   US-10-015-395A-276         Sequence 276, App
  3    3143   100.0   3143   13   US-10-006-485A-276         Sequence 276, App
  4    3143   100.0   3143   13   US-10-013-907A-276         Sequence 276, App
  5    3143   100.0   3143   13   US-10-015-499A-276         Sequence 276, App
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ALIGNMENTS

RESULT 1
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; Sequence 276, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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; PRIOR APPLICATION NUMBER: 60/099602
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099812
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;   PRIOR APPLICATION NUMBER: 60/099815
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099816
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/100385
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;   PRIOR APPLICATION NUMBER: 60/100388
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;   PRIOR FILING DATE: 1998-09-16
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;   PRIOR APPLICATION NUMBER: 60/100710
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;   PRIOR APPLICATION NUMBER: 60/100711
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;   PRIOR APPLICATION NUMBER: 60/100848
;   PRIOR FILING DATE: 1998-09-18
;   PRIOR APPLICATION NUMBER: 60/100849
;   PRIOR FILING DATE: 1998-09-18
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;   PRIOR APPLICATION NUMBER: 60/100930
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;   PRIOR APPLICATION NUMBER: 60/101068
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;   PRIOR FILING DATE: 1998-09-22
;   PRIOR APPLICATION NUMBER: 60/101471
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;   PRIOR APPLICATION NUMBER: 60/101472
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;   PRIOR APPLICATION NUMBER: 60/101474
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;   PRIOR APPLICATION NUMBER: 60/101475
;   PRIOR FILING DATE: 1998-09-23
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; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
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; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
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; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
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; PRIOR APPLICATION NUMBER: 60/103395
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; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
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; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633

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   Query Match              100.0%;  Score 3143;  DB 10;  Length 3143;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy        61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy       121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Db       121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy       181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Qy       241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
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Qy       301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db       301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy       361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Db      361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy      421  GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
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Db      421  GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy      481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
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Db      481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy      541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
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Db      541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy      601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
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Db      601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy      1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db      1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy      1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
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Db      1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy      1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
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Db      1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy      1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
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Db      1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
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Qy    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Db    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Db    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
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Db    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
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Db    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
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Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db    1741 CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
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Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
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Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Db  2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy  3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Db  3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy  3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Qy  3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Db  3121 TAAAAATATAAGGCTTAAAAAAA 3143


RESULT 2
US-10-015-395A-276
; Sequence 276, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C57
;  CURRENT APPLICATION NUMBER: US/10/015,395A
;  CURRENT FILING DATE:  2001-12-12
;  Prior application removed - See file Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-395A-276

  Query Match              100.0%;  Score 3143;  DB 12;  Length 3143;
  Best Local Similarity    100.0%;  Pred. No. 0;
  Matches 3143;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy    61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Qy        181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy        361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Db        361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy        421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
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Db        421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy        481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
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Db        481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy        541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
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Db        601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy        661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
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Db        661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy        721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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Db        721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy        781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
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Db        781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy        841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
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Db        841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy        901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
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Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
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Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
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Db     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
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Db     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
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Db     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

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Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Qy     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
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Qy     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Db     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy     1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db     1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Qy    1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
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Db    1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860

Qy    1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920
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Db    1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920

Qy    1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980
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Db    1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980

Qy    1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040
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Qy    2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
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Qy    2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160
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Qy    2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220
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Qy    2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
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Db    2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280

Qy    2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
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Qy    2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400
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Qy    2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460
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Db    2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460

Qy    2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520
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Db    2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520

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Qy    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640
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Db    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640
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Qy     2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db     2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy     2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db     2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy     2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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RESULT 3
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; Publication No. US20030064062A1
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan l.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth J.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
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Qy     301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy     361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy     421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
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               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601    AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy      661    CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661    CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy      721    CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721    CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781    GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781    GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841    TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841    TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901    CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901    CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961    TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961    TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy      1021   ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021   ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy      1081   CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081   CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy      1141   TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141   TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy      1201   CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201   CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy      1261   ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261   ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy      1321   CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321   CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy      1381   TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381   TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy      1441   CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy      1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy      1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy      1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy      1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy      1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy      1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860

Qy      1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920

Qy      1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980

Qy      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040

Qy      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100

Qy      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160

Qy      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220

Qy      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280

Qy      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
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Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Db   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Db   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Db   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 4
US-10-013-907A-276
; Sequence 276, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-013-907A-276

  Query Match   100.0%; Score 3143; DB 13; Length 3143;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

```
Qy   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGGCTCGAGAAGCCATTCTGG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGGCTCGAGAAGCCATTCTGG 360

Qy   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy   601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy   661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy   721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy   781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy   841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy   901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy   961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy  1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy  1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
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Db  1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy  1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
           |||||||||||||||||||||||
Db    3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 5
US-10-015-499A-276
; Sequence 276, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-499A-276

   Query Match   100.0%; Score 3143; DB 13; Length 3143;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1  GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC  60

Qy     61  ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC  120

Qy    121  TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC  180

Qy    181  TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG  240

Qy    241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300

Qy    301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360

Qy    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Qy     841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy     901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy     961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy    1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy    1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy    1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy    1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGGAACCCAGAGTGGG 1740
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy      1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy      1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860

Qy      1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920
                    |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920

Qy      1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980

Qy      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040

Qy      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100

Qy      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160

Qy      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220

Qy      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280

Qy      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340

Qy      2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400

Qy      2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460

Qy      2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520

Qy      2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580

Qy    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640

Qy    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700

Qy    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760

Qy    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820

Qy    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC  2880
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC  2880

Qy    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA  2940
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA  2940

Qy    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG  3000
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG  3000

Qy    3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC  3060
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC  3060

Qy    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT  3120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT  3120

Qy    3121  TAAAAATATAAGGCTTAAAAAAA  3143
            |||||||||||||||||||||||
Db    3121  TAAAAATATAAGGCTTAAAAAAA  3143
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RESULT 6
US-10-226-254A-276
; Sequence 276, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

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Query Match            100.0%;  Score 3143;  DB 13;  Length 3143;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 3143;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Qy    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
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Qy   1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
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                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1921   ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy        1981   CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1981   CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy        2041   CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2041   CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy        2101   CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2101   CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy        2161   CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2161   CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy        2221   CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2221   CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy        2281   AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2281   AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy        2341   CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2341   CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy        2401   CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2401   CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy        2461   TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2461   TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy        2521   TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2521   TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy        2581   TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2581   TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy        2641   TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2641   TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy        2701   CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        2701   CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy        2761   TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
                 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy      2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy      2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy      3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy      3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy      3121 TAAAAATATAAGGCTTAAAAAAA 3143
             |||||||||||||||||||||||
Db      3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 7
US-10-006-856A-276
; Sequence 276, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan l.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth J.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2830P1C14
;   CURRENT APPLICATION NUMBER: US/10/006,856A
;   CURRENT FILING DATE: 2002-05-10
;   NUMBER OF SEQ ID NOS: 477
;   Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens

Query Match   100.0%; Score 3143; DB 15; Length 3143;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy     61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy    121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy    181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy   1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
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Qy   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461   TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy     2521   TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521   TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy     2581   TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581   TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy     2641   TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641   TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy     2701   CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701   CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy     2761   TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2761   TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy     2821   AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2821   AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy     2881   TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2881   TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy     2941   CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2941   CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy     3001   CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3001   CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy     3061   TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3061   TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy     3121   TAAAAATATAAGGCTTAAAAAAA 3143
              |||||||||||||||||||||||
Db     3121   TAAAAATATAAGGCTTAAAAAAA 3143
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   Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy     481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy     541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy     601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy     661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy     721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy     781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy     841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy     901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy     961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy    1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy    1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy    1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy    1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
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Qy    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Db    3001   CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061   TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061   TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121   TAAAAATATAAGGCTTAAAAAAA 3143
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Db    3121   TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 9
US-10-015-393A-276
; Sequence 276, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-393A-276

   Query Match   100.0%; Score 3143; DB 15; Length 3143;
   Best Local Similarity 100.0%; Pred. No. 0;
   Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Db      121  TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC  180

Qy      181  TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG  240
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Db      181  TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG  240

Qy      241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300

Qy      301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360
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Db      301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360

Qy      361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy      421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy      481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy      541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy      601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy      1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy      1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy      1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy      1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy      1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Db      1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy      1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy      1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy      1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy      1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy      1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy      1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db      1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy      1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy      1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy      1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Qy      2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db      2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy      2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy      2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Db      2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy      2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy      3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Db      3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy      3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Db      3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy      3121 TAAAAATATAAGGCTTAAAAAAA 3143
             |||||||||||||||||||||||
Db      3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 10
US-10-015-869A-276
; Sequence 276, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25

    Query Match   100.0%;   Score 3143;   DB 15;   Length 3143;
    Best Local Similarity 100.0%;   Pred. No. 0;
    Matches 3143;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Qy   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
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Qy   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Qy   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
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Db   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

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Db   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
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Qy   601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
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Db   601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy   661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

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Qy       721    CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
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Db       721    CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy       781    GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Db       781    GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy       841    TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Db       841    TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy       901    CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
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Db       901    CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy       961    TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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Db       961    TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

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Db       1021   ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

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Qy       1201   CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
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Db       1201   CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy       1261   ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
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Db       1261   ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

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Qy       1441   CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
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Db   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

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Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
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Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

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Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

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Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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RESULT 11
US-10-012-121A-276
; Sequence 276, Application US/10012121A

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    Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
    Best Local Similarity    100.0%;  Pred. No. 0;
    Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy         241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
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Qy         301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
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Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
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Db    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

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Db    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
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Qy   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
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Qy   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
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Qy   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Db   1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Db   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Db   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
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Qy   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
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Db   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Db   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy   1741 CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db   1741 CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
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Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
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Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

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Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

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Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Qy      2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Qy      3121 TAAAAATATAAGGCTTAAAAAAA 3143
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; Publication No. US20030082626A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C15
;  CURRENT APPLICATION NUMBER: US/10/006,116A
;  CURRENT FILING DATE:  2001-12-16
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
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;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
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;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28

   Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
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   Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
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Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
```

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Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy   1741  CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
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                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy      1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860

Qy      1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920

Qy      1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980

Qy      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040

Qy      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100

Qy      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160

Qy      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220

Qy      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280

Qy      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340

Qy      2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400

Qy      2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460

Qy      2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520

Qy      2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580

Qy      2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121  TAAAAATATAAGGCTTAAAAAAA 3143
            |||||||||||||||||||||||
Db    3121  TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 13
US-10-006-117A-276
; Sequence 276, Application US/10006117A
; Publication No. US20030082627A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James

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   Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy      481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy      541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy     721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy     781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy     841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy     901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy     961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy    1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy    1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy    1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy    1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Qy    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Qy   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143

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RESULT 14
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; Sequence 276, Application US/10017527A
; Publication No. US20030082628A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C63
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
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; PRIOR APPLICATION NUMBER: 60/099741
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; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449

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Best Local Similarity  100.0%;  Pred. No. 0;
Matches 3143;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Db         1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy        61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy       121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Qy       181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Qy       241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
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Db     241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300

Qy     301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360
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Db     301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360

Qy     361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
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Db     361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy     421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
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Qy    .481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
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Db     481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy     541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
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Qy     601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
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Db     601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy     661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
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Qy     721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
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Db     721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy     781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Qy     841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Qy     901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
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Db     901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy     961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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Db     961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy    1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db    1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
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Db    1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

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Qy    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Qy      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040
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Db      1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040

Qy      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
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Db      2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100

Qy      2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160
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Qy      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220

Qy      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280

Qy      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340

Qy      2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400

Qy      2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460

Qy      2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520

Qy      2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580

Qy      2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640

Qy      2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700

Qy      2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760

Qy      2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820
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Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
           |||||||||||||||||||||||
Db    3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 15
US-10-013-913A-276
; Sequence 276, Application US/10013913A
; Publication No. US20030083462A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C40
; CURRENT APPLICATION NUMBER: US/10/013,913A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-013-913A-276

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Query Match          100.0%;  Score 3143;  DB 15;  Length 3143;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy     61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy    121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy    181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
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                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy      841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy      901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy      961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy     1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy     1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy     1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy     1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy     1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy     1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy     1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy     1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy     1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy     1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy     1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
          |||||||||||||||||||||||
Db   3121 TAAAAATATAAGGCTTAAAAAAA 3143


Search completed: May 13, 2004, 22:44:40
Job time : 1283 secs
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